OM protein - protein search, using sw model

Run on: May 15, 2006, 16:16:32 ; Search time 47 Seconds
(without alignments)
28.145 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	100.0	16	2	US-09-070-907-1	Sequence 1, Appli
2	91	100.0	16	2	US-09-623-548A-1536	Sequence 1536, Ap
3	91	100.0	16	2	US-09-657-276-1536	Sequence 1536, Ap
4	91	100.0	63	1	US-08-447-411-24	Sequence 24, Appl
5	91	100.0	63	1	US-08-447-411-63	Sequence 63, Appl
6	91	100.0	63	1	US-08-662-227-20	Sequence 20, Appl
7	91	100.0	63	2	US-09-017-947-20	Sequence 20, Appl
8	91	100.0	63	2	US-09-925-442-20	Sequence 20, Appl
9	91	100.0	310	2	US-09-834-309-7	Sequence 7, Appli
10	91	100.0	310	2	US-09-834-309-8	Sequence 8, Appli
11	91	100.0	310	2	US-09-834-309-9	Sequence 9, Appli
12	91	100.0	1663	1	US-08-793-126-1	Sequence 1, Appli
13	91	100.0	1663	2	US-09-132-271-1	Sequence 1, Appli
14	91	100.0	1663	2	US-09-142-334-22	Sequence 22, Appl
15	80	87.9	63	1	US-08-447-411-26	Sequence 26, Appl
16	79	86.8	63	1	US-08-447-411-27	Sequence 27, Appl
17	73	80.2	63	1	US-08-447-411-25	Sequence 25, Appl
18	73	80.2	308	2	US-09-582-761B-26	Sequence 26, Appl
19	73	80.2	330	2	US-09-582-761B-37	Sequence 37, Appl
20	73	80.2	929	2	US-09-582-761B-27	Sequence 27, Appl
21	60	65.9	11	2	US-09-039-060A-6	Sequence 6, Appli
22	60	65.9	11	2	US-08-495-606E-37	Sequence 37, Appl
23	60	65.9	11	4	PCT-US94-01234-37	Sequence 37, Appl
24	60	65.9	11	4	PCT-US94-01263-7	Sequence 7, Appli
25	52	57.1	1333	1	US-08-447-411-76	Sequence 76, Appl
26	52	57.1	1333	1	US-08-662-227-34	Sequence 34, Appl
27	52	57.1	1333	2	US-09-017-947-34	Sequence 34, Appl
28	52	57.1	1333	2	US-09-925-442-34	Sequence 34, Appl
29	51	56.0	10	1	US-08-634-060-33	Sequence 33, Appl
30	51	56.0	10	1	US-08-700-846-5	Sequence 5, Appli
31	46	50.5	1493	2	US-09-713-273A-20	Sequence 20, Appl
32	44	48.4	193	2	US-09-248-796A-20794	Sequence 20794, A
33	44	48.4	2628	2	US-09-413-814-11	Sequence 11, Appl
34	43	47.3	28	1	US-08-448-603A-7	Sequence 7, Appli
35	43	47.3	28	2	US-09-134-075-7	Sequence 7, Appli
36	43	47.3	28	2	US-09-492-739-7	Sequence 7, Appli
37	43	47.3	28	2	US-09-966-931A-7	Sequence 7, Appli
38	43	47.3	63	1	US-08-447-411-23	Sequence 23, Appl
39	43	47.3	63	1	US-08-447-411-62	Sequence 62, Appl
40	43	47.3	63	1	US-08-662-227-19	Sequence 19, Appl
41	43	47.3	63	2	US-09-017-947-19	Sequence 19, Appl
42	43	47.3	63	2	US-09-925-442-19	Sequence 19, Appl
43	43	47.3	95	2	US-09-270-767-39763	Sequence 39763, A
44	43	47.3	95	2	US-09-270-767-54980	Sequence 54980, A
45	43	47.3	467	2	US-10-040-802-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-070-907-1
; Sequence 1, Application US/09070907
; Patent No. 6238667
; GENERAL INFORMATION:
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: METHOD OF AFFINITY CROSS-LINKING BIOLOGICALLY ACTIVE
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES TO ANTIBODIES.
; FILE REFERENCE: 35629
; CURRENT APPLICATION NUMBER: US/09/070,907
; CURRENT FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AMINO ACID
; OTHER INFORMATION: SEQUENCE DERIVED FROM Cd3 peptide
US-09-070-907-1

Query Match 100.0%; Score 91; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
||||||||||||||||
Db 1 KNRWEDPGKQLYNVEA 16

RESULT 2
US-09-623-548A-1536
; Sequence 1536, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17

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;  PRIOR APPLICATION NUMBER: 60/153,406
;  PRIOR FILING DATE: 1999-09-10
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-18
;  NUMBER OF SEQ ID NOS: 1617
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1536
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-623-548A-1536

  Query Match             100.0%;  Score 91;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-09;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16


RESULT 3
US-09-657-276-1536
; Sequence 1536, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
;  APPLICANT:  Conjuchem, Inc.
;  APPLICANT:  Bridon, Dominique
;  APPLICANT:  Ezrin, Alan
;  APPLICANT:  Milner, Peter
;  APPLICANT:  Holmes, Darren
;  APPLICANT:  Thibaudeau, Karen
;  TITLE OF INVENTION:  PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;  TITLE OF INVENTION:  PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;  TITLE OF INVENTION:  COMPONENTS
;  FILE REFERENCE:  2110
;  CURRENT APPLICATION NUMBER: US/09/657,276
;  CURRENT FILING DATE:  2000-09-07
;  PRIOR APPLICATION NUMBER:  60/134,406
;  PRIOR FILING DATE:  1999-05-17
;  PRIOR APPLICATION NUMBER:  60/153,406
;  PRIOR FILING DATE:  1999-09-10
;  PRIOR APPLICATION NUMBER:  60/159,783
;  PRIOR FILING DATE:  1999-10-18
;  NUMBER OF SEQ ID NOS:  1617
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1536
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-657-276-1536

  Query Match             100.0%;  Score 91;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-09;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16


RESULT 4
US-08-447-411-24
; Sequence 24, Application US/08447411
; Patent No. 5773243
;  GENERAL INFORMATION:
;    APPLICANT:  FRITZINGER, DAVID C.
;    APPLICANT:  BREDEHORST, REINHARD
;    APPLICANT:  VOGEL, CARL-WILHELM
;    TITLE OF INVENTION:  DNA ENCODING COBRA C3, CVF1, AND CVF2
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,411
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/043,747
;      FILING DATE:  07-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5773243man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  1126-101-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  63 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-447-411-24

  Query Match             100.0%;  Score 91;  DB 1;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          9 KNRWEDPGKQLYNVEA 24


RESULT 5
US-08-447-411-63
; Sequence 63, Application US/08447411
; Patent No. 5773243
;  GENERAL INFORMATION:
;    APPLICANT:  FRITZINGER, DAVID C.
;    APPLICANT:  BREDEHORST, REINHARD
;    APPLICANT:  VOGEL, CARL-WILHELM
;    TITLE OF INVENTION:  DNA ENCODING COBRA C3, CVF1, AND CVF2
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/447,411
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/043,747
;       FILING DATE:  07-APR-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Oblon, No. 5773243man F.
;       REGISTRATION NUMBER:  24,618
;       REFERENCE/DOCKET NUMBER:  1126-101-0
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 413-3000
;       TELEFAX:  (703) 413-2220
;       TELEX:  248855 OPAT UR
;   INFORMATION FOR SEQ ID NO:  63:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  63 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
US-08-447-411-63

  Query Match             100.0%;  Score 91;  DB 1;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          9 KNRWEDPGKQLYNVEA 24


RESULT 6
US-08-662-227-20
; Sequence 20, Application US/08662227
; Patent No. 5922320
;  GENERAL INFORMATION:
;    APPLICANT:  VOGEL, CARL-WILHELM
;    APPLICANT:  BREDEHORST, REINHORST
;    APPLICANT:  KOCK, MICHAEL
;    APPLICANT:  FRITZINGER, DAVID
;    TITLE OF INVENTION:  RECOMBINANT PROCVF
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/662,227
;      FILING DATE:  14-JUN-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  1126-0107-0X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  63 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-662-227-20

  Query Match             100.0%;  Score 91;  DB 1;  Length 63;
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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          9 KNRWEDPGKQLYNVEA 24


RESULT 7
US-09-017-947-20
; Sequence 20, Application US/09017947
; Patent No. 6303754
;  GENERAL INFORMATION:
;    APPLICANT:  VOGEL, CARL-WILHELM
;    APPLICANT:  BREDEHORST, REINHORST
;    APPLICANT:  KOCK, MICHAEL
;    APPLICANT:  FRITZINGER, DAVID
;    TITLE OF INVENTION:  RECOMBINANT PROCVF
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/017,947
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/662,227
;      FILING DATE:  14-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  1126-0107-0X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  63 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-017-947-20

  Query Match             100.0%;  Score 91;  DB 2;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          9 KNRWEDPGKQLYNVEA 24


RESULT 8
US-09-925-442-20
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; Sequence 20, Application US/09925442
; Patent No. 6607897
;   GENERAL INFORMATION:
;        APPLICANT: VOGEL, CARL-WILHELM
;                   BREDEHORST, REINHORST
;                   KOCK, MICHAEL
;                   FRITZINGER, DAVID
;        TITLE OF INVENTION: RECOMBINANT PROCVF
;        NUMBER OF SEQUENCES: 39
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;                        P.C.
;             STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22202
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/925,442
;             FILING DATE: 10-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/017,947
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: OBLON, NORMAN F.
;             REGISTRATION NUMBER: 24,618
;             REFERENCE/DOCKET NUMBER: 1126-0107-0X
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 703-413-3000
;             TELEFAX: 703-413-2220
;   INFORMATION FOR SEQ ID NO: 20:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 63 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-925-442-20

  Query Match             100.0%;  Score 91;  DB 2;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          9 KNRWEDPGKQLYNVEA 24


RESULT 9
US-09-834-309-7
; Sequence 7, Application US/09834309
; Patent No. 6820011
; GENERAL INFORMATION:
;  APPLICANT: Chen, Xiaojiang
;  APPLICANT:  Holers, V. Michael
;  TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2848-43
;  CURRENT APPLICATION NUMBER: US/09/834,309
;  CURRENT FILING DATE:  2001-04-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-309-7

  Query Match             100.0%;  Score 91;  DB 2;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
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Db        224 KNRWEDPGKQLYNVEA 239


RESULT 10
US-09-834-309-8
; Sequence 8, Application US/09834309
; Patent No. 6820011
; GENERAL INFORMATION:
;  APPLICANT: Chen, Xiaojiang
;  APPLICANT:  Holers, V. Michael
;  TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND US
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2848-43
;  CURRENT APPLICATION NUMBER: US/09/834,309
;  CURRENT FILING DATE:  2001-04-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-309-8

  Query Match             100.0%;  Score 91;  DB 2;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 11
US-09-834-309-9
; Sequence 9, Application US/09834309
; Patent No. 6820011
; GENERAL INFORMATION:
;  APPLICANT: Chen, Xiaojiang
;  APPLICANT:  Holers, V. Michael
;  TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND US
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2848-43
;  CURRENT APPLICATION NUMBER: US/09/834,309
;  CURRENT FILING DATE:  2001-04-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-309-9

  Query Match             100.0%;  Score 91;  DB 2;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 12
US-08-793-126-1
; Sequence 1, Application US/08793126
; Patent No. 5849297
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Harrison; Richard Alexander
;    APPLICANT:  Farries, Charles Timothy
;    TITLE OF INVENTION:  MODIFIED HUMAN C3 PROTEINS
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HALE AND DORR LLP
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  United States of America
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,126
;      FILING DATE:  07-FEB-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Baker, Hollie L.
;      REGISTRATION NUMBER:  31,321
;      REFERENCE/DOCKET NUMBER:  102286.377
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 526-6000
;      TELEFAX:  (617) 526-5000
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1663 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-793-126-1

  Query Match             100.0%;  Score 91;  DB 1;  Length 1663;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db       1217 KNRWEDPGKQLYNVEA 1232


RESULT 13
US-09-132-271-1
; Sequence 1, Application US/09132271
; Patent No. 6221657
;  GENERAL INFORMATION:
;    APPLICANT:  Harrison, Richard Alexander
;    APPLICANT:  Farries, Charles Timothy
;    TITLE OF INVENTION:  MODIFIED HUMAN C3 PROTEINS
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HALE AND DORR LLP
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  United States of America
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/132,271
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/793,126
;      FILING DATE:  07-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Baker, Hollie L.
;      REGISTRATION NUMBER:  31,321
;      REFERENCE/DOCKET NUMBER:  102286.377
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 526-6000
;      TELEFAX:  (617) 526-5000
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1663 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-132-271-1

  Query Match             100.0%;  Score 91;  DB 2;  Length 1663;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db       1217 KNRWEDPGKQLYNVEA 1232


RESULT 14
US-09-142-334-22
; Sequence 22, Application US/09142334
; Patent No. 6268485
; GENERAL INFORMATION:
;  APPLICANT: Farries, Timothy C.
;  APPLICANT: Harrison, Richard A.
;  TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
;  FILE REFERENCE: 4-30443/A/IMU/PCT
;  CURRENT APPLICATION NUMBER: US/09/142,334
;  CURRENT FILING DATE: 1999-04-15
;  EARLIER APPLICATION NUMBER: PCT/GB97/00603
;  EARLIER FILING DATE: 1997-03-04
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;    LENGTH: 1663
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-142-334-22

  Query Match             100.0%;  Score 91;  DB 2;  Length 1663;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db       1217 KNRWEDPGKQLYNVEA 1232


RESULT 15
US-08-447-411-26
; Sequence 26, Application US/08447411
; Patent No. 5773243
;  GENERAL INFORMATION:
;    APPLICANT:  FRITZINGER, DAVID C.
;    APPLICANT:  BREDEHORST, REINHARD
;    APPLICANT:  VOGEL, CARL-WILHELM
;    TITLE OF INVENTION:  DNA ENCODING COBRA C3, CVF1, AND CVF2
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
```

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;       ZIP:  22202
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/447,411
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/043,747
;       FILING DATE:  07-APR-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Oblon, No. 5773243man F.
;       REGISTRATION NUMBER:  24,618
;       REFERENCE/DOCKET NUMBER:  1126-101-0
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 413-3000
;       TELEFAX:  (703) 413-2220
;       TELEX:  248855 OPAT UR
;   INFORMATION FOR SEQ ID NO:  26:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  63 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-447-411-26

  Query Match             87.9%;  Score 80;  DB 1;  Length 63;
  Best Local Similarity   81.2%;  Pred. No. 2.7e-06;
  Matches   13;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              :||||:||:|||||||
Db          9 RNRWEEPGQQLYNVEA 24


Search completed: May 15, 2006, 16:17:50
Job time : 48 secs
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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:27:41 ; Search time 164 Seconds
(without alignments)
40.764 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	100.0	16	3	US-09-865-281A-1	Sequence 1, Appli
2	91	100.0	16	5	US-10-795-081A-1	Sequence 1, Appli
3	91	100.0	16	6	US-11-066-697-1536	Sequence 1536, Ap
4	91	100.0	63	3	US-09-925-442-20	Sequence 20, Appl
5	91	100.0	94	4	US-10-424-599-219407	Sequence 219407,
6	91	100.0	310	3	US-09-834-309-7	Sequence 7, Appli
7	91	100.0	310	3	US-09-834-309-8	Sequence 8, Appli
8	91	100.0	310	3	US-09-834-309-9	Sequence 9, Appli
9	91	100.0	705	4	US-10-379-747-4	Sequence 4, Appli
10	91	100.0	935	5	US-10-887-775-32	Sequence 32, Appl
11	91	100.0	1255	5	US-10-497-073-17	Sequence 17, Appl
12	91	100.0	1288	5	US-10-741-600-1326	Sequence 1326, Ap
13	91	100.0	1540	5	US-10-450-763-56335	Sequence 56335, A
14	91	100.0	1638	5	US-10-884-813-8	Sequence 8, Appli
15	91	100.0	1638	5	US-10-884-813-12	Sequence 12, Appl
16	91	100.0	1663	3	US-09-875-519A-22	Sequence 22, Appl
17	91	100.0	1663	3	US-09-842-758-41	Sequence 41, Appl
18	91	100.0	1663	4	US-10-379-747-2	Sequence 2, Appli
19	91	100.0	1663	4	US-10-174-333-41	Sequence 41, Appl
20	91	100.0	1663	5	US-10-741-600-1327	Sequence 1327, Ap
21	91	100.0	1663	5	US-10-928-312-2	Sequence 2, Appli
22	91	100.0	1663	5	US-10-884-813-2	Sequence 2, Appli
23	91	100.0	1663	5	US-10-884-813-6	Sequence 6, Appli
24	91	100.0	1663	5	US-10-884-813-10	Sequence 10, Appl
25	91	100.0	1663	5	US-10-887-775-30	Sequence 30, Appl
26	83	91.2	296	4	US-10-398-916-29	Sequence 29, Appl
27	83	91.2	296	4	US-10-398-916-30	Sequence 30, Appl
28	83	91.2	300	4	US-10-398-916-13	Sequence 13, Appl
29	82	90.1	105	3	US-09-925-301-1490	Sequence 1490, Ap
30	80	87.9	1663	5	US-10-989-891-141	Sequence 141, App
31	76	83.5	300	4	US-10-398-916-11	Sequence 11, Appl
32	76	83.5	300	4	US-10-398-916-15	Sequence 15, Appl
33	73	80.2	300	4	US-10-398-916-9	Sequence 9, Appli
34	73	80.2	312	4	US-10-398-916-17	Sequence 17, Appl
35	73	80.2	409	4	US-10-466-655-6	Sequence 6, Appli
36	73	80.2	1663	3	US-09-842-758-43	Sequence 43, Appl
37	73	80.2	1663	4	US-10-174-333-43	Sequence 43, Appl
38	71	78.0	1661	3	US-09-842-758-42	Sequence 42, Appl
39	71	78.0	1661	4	US-10-174-333-42	Sequence 42, Appl
40	69	75.8	296	5	US-10-505-546-10	Sequence 10, Appl
41	60	65.9	11	4	US-10-408-849-6	Sequence 6, Appli
42	52	57.1	1333	3	US-09-925-442-34	Sequence 34, Appl
43	46.5	51.1	500	4	US-10-282-122A-57243	Sequence 57243, A
44	46	50.5	329	4	US-10-425-115-197051	Sequence 197051,
45	46	50.5	437	4	US-10-424-599-190068	Sequence 190068,

ALIGNMENTS

RESULT 1
US-09-865-281A-1
; Sequence 1, Application US/09865281A
; Publication No. US20030103984A1
; GENERAL INFORMATION:
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: FUSION PROTEINS OF BIOLOGICALLY ACTIVE PEPTIDES AND ANTIBODIES
; FILE REFERENCE: 411.35629PC2
; CURRENT APPLICATION NUMBER: US/09/865,281A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/070,907
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Synthesized peptide with sequence derived from position 1217-123
US-09-865-281A-1

Query Match 100.0%; Score 91; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
||||||||||||||||
Db 1 KNRWEDPGKQLYNVEA 16

RESULT 2
US-10-795-081A-1
; Sequence 1, Application US/10795081A
; Publication No. US20050033033A1
; GENERAL INFORMATION:
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: TRANS-MEMBRANE-ANTIBODY INDUCED INHIBITION OF APOPTOSIS
; FILE REFERENCE: 411.35629AP3
; CURRENT APPLICATION NUMBER: US/10/795,081A
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 60/451,980
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 09/865,281
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/070,907
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 14

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;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Synthesized peptide with sequence derived from position 1217-1232
US-10-795-081A-1

  Query Match             100.0%;  Score 91;  DB 5;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16


RESULT 3
US-11-066-697-1536
; Sequence 1536, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Milner, Peter G.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Thibaudeau, Karen
;  TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;  TITLE OF INVENTION:  PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;  TITLE OF INVENTION:  COMPONENTS
;  FILE REFERENCE: 500862002301
;  CURRENT APPLICATION NUMBER: US/11/066,697
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: 09/657,276
;  PRIOR FILING DATE: 2000-09-07
;  PRIOR APPLICATION NUMBER: 60/153,406
;  PRIOR FILING DATE: 1999-09-10
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  NUMBER OF SEQ ID NOS: 1617
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1536
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-066-697-1536

  Query Match             100.0%;  Score 91;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16


RESULT 4
US-09-925-442-20
; Sequence 20, Application US/09925442
; Patent No. US20020103346A1
;   GENERAL INFORMATION:
;        APPLICANT: VOGEL, CARL-WILHELM
;                   BREDEHORST, REINHORST
;                   KOCK, MICHAEL
;                   FRITZINGER, DAVID
;        TITLE OF INVENTION: RECOMBINANT PROCVF
;        NUMBER OF SEQUENCES: 39
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;                        P.C.
;             STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22202
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/925,442
;             FILING DATE: 10-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/017,947
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: OBLON, NORMAN F.
;             REGISTRATION NUMBER: 24,618
;             REFERENCE/DOCKET NUMBER: 1126-0107-0X
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 703-413-3000
;             TELEFAX: 703-413-2220
;   INFORMATION FOR SEQ ID NO: 20:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 63 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-925-442-20

  Query Match             100.0%;  Score 91;  DB 3;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          9 KNRWEDPGKQLYNVEA 24


RESULT 5
US-10-424-599-219407
; Sequence 219407, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 219407
;   LENGTH: 94
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(94)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_40150C.1.pep
US-10-424-599-219407
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  Query Match           100.0%;  Score 91;  DB 4;  Length 94;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db         43 KNRWEDPGKQLYNVEA 58


RESULT 6
US-09-834-309-7
; Sequence 7, Application US/09834309
; Publication No. US20040005538A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Xiaojiang
;  APPLICANT:  Holers, V. Michael
;  TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2848-43
;  CURRENT APPLICATION NUMBER: US/09/834,309
;  CURRENT FILING DATE:  2001-04-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-309-7

  Query Match           100.0%;  Score 91;  DB 3;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 7
US-09-834-309-8
; Sequence 8, Application US/09834309
; Publication No. US20040005538A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Xiaojiang
;  APPLICANT:  Holers, V. Michael
;  TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2848-43
;  CURRENT APPLICATION NUMBER: US/09/834,309
;  CURRENT FILING DATE:  2001-04-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-309-8

  Query Match           100.0%;  Score 91;  DB 3;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 8
US-09-834-309-9
; Sequence 9, Application US/09834309
; Publication No. US20040005538A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Xiaojiang
;  APPLICANT:  Holers, V. Michael
;  TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2848-43
;  CURRENT APPLICATION NUMBER: US/09/834,309
;  CURRENT FILING DATE:  2001-04-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-834-309-9

  Query Match           100.0%;  Score 91;  DB 3;  Length 310;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 9
US-10-379-747-4
; Sequence 4, Application US/10379747
; Publication No. US20040023874A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E.;
;  APPLICANT:  Chant, John S.;
;  APPLICANT:  Chaudhuri, Amitabha ;
;  APPLICANT:  Edinger, Shlomit R.;
;  APPLICANT:  Gangolli, Esha A.;
;  APPLICANT:  Malyankar, Uriel M.;
;  APPLICANT:  Miller, Charles E.;
;  APPLICANT:  Ooi, Chean Eng;
;  APPLICANT:  Ort, Tatiana A.;
;  APPLICANT:  Patturajan, Meera ;
;  APPLICANT:  Rastelli, Luca ;
;  APPLICANT:  Rieger, Daniel K.;
;  APPLICANT:  Shimkets, Richard A.;
;  APPLICANT:  Zerhusen, Bryan D.
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
;  FILE REFERENCE: 21402-568B
;  CURRENT APPLICATION NUMBER: US/10/379,747
;  CURRENT FILING DATE:  2003-03-05
;  PRIOR APPLICATION NUMBER: 60/365,034
;  PRIOR FILING DATE: 2002-03-15
;  PRIOR APPLICATION NUMBER: 60/366,420
;  PRIOR FILING DATE: 2002-03-21
;  PRIOR APPLICATION NUMBER: 60/365,477
;  PRIOR FILING DATE: 2002-03-19
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
;   LENGTH: 705
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-379-747-4

  Query Match           100.0%;  Score 91;  DB 4;  Length 705;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
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Db        259 KNRWEDPGKQLYNVEA 274


RESULT 10
US-10-887-775-32
; Sequence 32, Application US/10887775
; Publication No. US20050130182A1
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; GENERAL INFORMATION:
;  APPLICANT: MESSER, Jeffrey
;  APPLICANT:  BENJAMIN, Dennis
;  APPLICANT:  VATH, James
;  APPLICANT:  SIGEL, Eric
;  TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  ENDOMETRIOSIS
;  FILE REFERENCE: PPI-149
;  CURRENT APPLICATION NUMBER: US/10/887,775
;  CURRENT FILING DATE:  2004-07-09
;  PRIOR APPLICATION NUMBER: 60/486,379
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: 60/533,430
;  PRIOR FILING DATE: 2003-12-29
;  PRIOR APPLICATION NUMBER: 60/575,269
;  PRIOR FILING DATE: 2004-05-08
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 935
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-887-775-32

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  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
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Db        489 KNRWEDPGKQLYNVEA 504


RESULT 11
US-10-497-073-17
; Sequence 17, Application US/10497073
; Publication No. US20050048584A1
; GENERAL INFORMATION:
;  APPLICANT: BioVision AG
;  TITLE OF INVENTION: Method for detecting Alzheimer's disease and differentiating
;  TITLE OF INVENTION:  Alzheimer's disease from other demential diseases, associated
;  TITLE OF INVENTION:  peptides and the use thereof
;  FILE REFERENCE: C3f-PCT
;  CURRENT APPLICATION NUMBER: US/10/497,073
;  CURRENT FILING DATE:  2004-05-28
;  PRIOR APPLICATION NUMBER: DE10158180
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: PCT/DE02/04360
;  PRIOR FILING DATE: 2002-11-27
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 1255
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-497-073-17

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  Best Local Similarity   100.0%;  Pred. No. 1.6e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        809 KNRWEDPGKQLYNVEA 824


RESULT 12
US-10-741-600-1326
; Sequence 1326, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1326
;   LENGTH: 1288
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-600-1326

  Query Match            100.0%;  Score 91;  DB 5;  Length 1288;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db       1217 KNRWEDPGKQLYNVEA 1232


RESULT 13
US-10-450-763-56335
; Sequence 56335, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;  FILE REFERENCE: 790CIP3/US
;  CURRENT APPLICATION NUMBER: US/10/450,763
;  CURRENT FILING DATE:  2003-06-11
;  PRIOR APPLICATION NUMBER: PCT/US01/08631
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 60736
;  SOFTWARE: Custom
; SEQ ID NO 56335
;   LENGTH: 1540
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (689)..(699)
;   OTHER INFORMATION: ANAPHYLATOXIN DOMAIN SIGNATURE domain identified by eMATRIX,
;   OTHER INFORMATION: accession number PR00004A, p-value=5.500e-13, raw score of 9.52
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (756)..(1370)
;   OTHER INFORMATION: Alpha-2-macroglobulin family domain identified by PFam,
;   OTHER INFORMATION: accession name A2M, E-value=0, PFam score of 1156.5
US-10-450-763-56335

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  Best Local Similarity   100.0%;  Pred. No. 1.9e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db       1217 KNRWEDPGKQLYNVEA 1232


RESULT 14
US-10-884-813-8
; Sequence 8, Application US/10884813
; Publication No. US20050079585A1
; GENERAL INFORMATION:
;  APPLICANT: Kolln, Johanna
;  APPLICANT:  Bredehorst, Reinhard
;  APPLICANT:  Spillner, Edzard
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;  TITLE OF INVENTION: Complement Depletion with Recombinant Human C3 Derivatives
;  FILE REFERENCE: P 63782
;  CURRENT APPLICATION NUMBER: US/10/884,813
;  CURRENT FILING DATE:  2004-07-02
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 1638
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Hybrid protein
US-10-884-813-8

  Query Match             100.0%;  Score 91;  DB 5;  Length 1638;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db       1217 KNRWEDPGKQLYNVEA 1232


RESULT 15
US-10-884-813-12
; Sequence 12, Application US/10884813
; Publication No. US20050079585A1
; GENERAL INFORMATION:
;  APPLICANT: Kolln, Johanna
;  APPLICANT:  Bredehorst, Reinhard
;  APPLICANT:  Spillner, Edzard
;  TITLE OF INVENTION: Complement Depletion with Recombinant Human C3 Derivatives
;  FILE REFERENCE: P 63782
;  CURRENT APPLICATION NUMBER: US/10/884,813
;  CURRENT FILING DATE:  2004-07-02
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 1638
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Hybrid protein
US-10-884-813-12

  Query Match             100.0%;  Score 91;  DB 5;  Length 1638;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db       1217 KNRWEDPGKQLYNVEA 1232


Search completed: May 15, 2006, 16:31:27
Job time : 165 secs
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GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 15, 2006, 16:31:41 ; Search time 28 Seconds
(without alignments)
26.828 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep1:*
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4: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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12: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	100.0	310	9	US-10-921-415-7	Sequence 7, Appli
2	91	100.0	310	9	US-10-921-415-8	Sequence 8, Appli
3	91	100.0	310	9	US-10-921-415-9	Sequence 9, Appli
4	91	100.0	1663	9	US-10-982-545-6	Sequence 6, Appli
5	91	100.0	1663	11	US-11-177-506-34	Sequence 34, Appl
6	73	80.2	300	8	US-10-514-462-11	Sequence 11, Appl
7	43	47.3	347	11	US-11-079-463-5775	Sequence 5775, Ap
8	43	47.3	499	9	US-10-514-055-5	Sequence 5, Appli
9	43	47.3	591	11	US-11-188-298-713	Sequence 713, App
10	43	47.3	591	11	US-11-188-298-8505	Sequence 8505, Ap
11	43	47.3	591	11	US-11-188-298-10639	Sequence 10639, A
12	43	47.3	591	11	US-11-188-298-13585	Sequence 13585, A
13	43	47.3	655	11	US-11-188-298-1487	Sequence 1487, Ap
14	43	47.3	842	11	US-11-100-356-2	Sequence 2, Appli
15	43	47.3	847	8	US-10-514-462-1	Sequence 1, Appli
16	42	46.2	374	9	US-10-517-939-340	Sequence 340, App
17	42	46.2	374	9	US-10-517-939-356	Sequence 356, App
18	40	44.0	189	9	US-10-506-454-336	Sequence 336, App
19	39	42.9	83	9	US-10-934-944-347	Sequence 347, App
20	39	42.9	83	9	US-10-934-944-348	Sequence 348, App
21	39	42.9	83	11	US-11-116-881A-2244	Sequence 2244, Ap
22	39	42.9	83	11	US-11-116-881A-2245	Sequence 2245, Ap
23	39	42.9	191	11	US-11-188-298-11339	Sequence 11339, A
24	39	42.9	250	11	US-11-096-568A-31657	Sequence 31657, A
25	39	42.9	302	11	US-11-096-568A-31656	Sequence 31656, A
26	39	42.9	320	11	US-11-079-463-8514	Sequence 8514, Ap
27	39	42.9	326	11	US-11-024-959-327	Sequence 327, App
28	39	42.9	355	11	US-11-188-298-4023	Sequence 4023, Ap
29	39	42.9	479	9	US-10-517-939-250	Sequence 250, App
30	39	42.9	513	11	US-11-188-298-12438	Sequence 12438, A
31	39	42.9	521	11	US-11-087-099-6169	Sequence 6169, Ap
32	39	42.9	521	11	US-11-188-298-14318	Sequence 14318, A
33	39	42.9	525	9	US-10-934-944-170	Sequence 170, App
34	39	42.9	525	9	US-10-934-944-188	Sequence 188, App
35	39	42.9	525	11	US-11-116-881A-179	Sequence 179, App
36	39	42.9	525	11	US-11-116-881A-197	Sequence 197, App
37	39	42.9	832	11	US-11-108-172-1081	Sequence 1081, Ap
38	39	42.9	958	11	US-11-108-172-1087	Sequence 1087, Ap
39	39	42.9	1128	11	US-11-079-463-9398	Sequence 9398, Ap
40	38.5	42.3	166	11	US-11-079-463-6057	Sequence 6057, Ap
41	38.5	42.3	336	11	US-11-096-568A-7234	Sequence 7234, Ap
42	38.5	42.3	341	11	US-11-096-568A-7233	Sequence 7233, Ap
43	38.5	42.3	355	11	US-11-096-568A-7232	Sequence 7232, Ap
44	38.5	42.3	917	11	US-11-188-298-3936	Sequence 3936, Ap
45	38	41.8	336	11	US-11-129-143-105	Sequence 105, App

ALIGNMENTS

RESULT 1
US-10-921-415-7
; Sequence 7, Application US/10921415
; Publication No. US20060014681A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Xiaojiang
; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/10/921,415
; CURRENT FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: US/09/834,309
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-415-7

Query Match 100.0%; Score 91; DB 9; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
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Db 224 KNRWEDPGKQLYNVEA 239

RESULT 2
US-10-921-415-8
; Sequence 8, Application US/10921415
; Publication No. US20060014681A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Xiaojiang
; APPLICANT: Holers, V. Michael
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 2848-43
; CURRENT APPLICATION NUMBER: US/10/921,415
; CURRENT FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: US/09/834,309

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;  PRIOR FILING DATE: 2001-04-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-921-415-8

  Query Match             100.0%;  Score 91;  DB 9;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
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Db        224 KNRWEDPGKQLYNVEA 239


RESULT 3
US-10-921-415-9
; Sequence 9, Application US/10921415
; Publication No. US20060014681A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Xiaojiang
;  APPLICANT:  Holers, V. Michael
;  TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 2848-43
;  CURRENT APPLICATION NUMBER: US/10/921,415
;  CURRENT FILING DATE:  2004-08-16
;  PRIOR APPLICATION NUMBER: US/09/834,309
;  PRIOR FILING DATE: 2001-04-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-921-415-9

  Query Match             100.0%;  Score 91;  DB 9;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 4
US-10-982-545-6
; Sequence 6, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
;  APPLICANT: Davies, Huw Alun
;  APPLICANT:  McGuire, James
;  APPLICANT:  Simonsen, Anja Hviid
;  APPLICANT:  Blennow, Kaj
;  APPLICANT:  Podust, Vladimir
;  APPLICANT:  Ciphergen Biosystems, Inc.
;  TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
;  FILE REFERENCE: 016866-011550US
;  CURRENT APPLICATION NUMBER: US/10/982,545
;  CURRENT FILING DATE:  2004-11-06
;  PRIOR APPLICATION NUMBER: US 60/518,360
;  PRIOR FILING DATE: 2003-11-07
;  PRIOR APPLICATION NUMBER: US 60/526,753
;  PRIOR FILING DATE: 2003-12-02
;  PRIOR APPLICATION NUMBER: US 60/546,423
;  PRIOR FILING DATE: 2004-02-19
;  PRIOR APPLICATION NUMBER: US 60/547,250
;  PRIOR FILING DATE: 2004-02-23
;  PRIOR APPLICATION NUMBER: US 60/558,896
;  PRIOR FILING DATE: 2004-04-02
;  PRIOR APPLICATION NUMBER: US 60/572,617
;  PRIOR FILING DATE: 2004-05-18
;  PRIOR APPLICATION NUMBER: US 60/586,503
;  PRIOR FILING DATE: 2004-07-08
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 1663
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: complement component C3 precursor
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)..(23)
;   OTHER INFORMATION: signal peptide
;   FEATURE:
;   NAME/KEY: CHAIN
;   LOCATION: (23)..(667)
;   OTHER INFORMATION: complement component C3 beta-chain
;   FEATURE:
;   NAME/KEY: CHAIN
;   LOCATION: (672)..(1663)
;   OTHER INFORMATION: complement component C3 alpha-chain
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (672)..(748)
;   OTHER INFORMATION: C3a anaphylatoxin peptide
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (672)..(747)
;   OTHER INFORMATION: biomarker peptide M8933.2, C3a anaphylatoxin
;   OTHER INFORMATION: desArg peptide
US-10-982-545-6

  Query Match             100.0%;  Score 91;  DB 9;  Length 1663;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db       1217 KNRWEDPGKQLYNVEA 1232


RESULT 5
US-11-177-506-34
; Sequence 34, Application US/11177506
; Publication No. US20060029956A1
; GENERAL INFORMATION:
;  APPLICANT: Beyer, Wayne F.
;  APPLICANT:  Venetta, Thomas M.
;  APPLICANT:  Groelke, John W.
;  APPLICANT:  Blaesius, Rainer H.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
;  TITLE OF INVENTION:  DETECTION OF OVARIAN DISEASE
;  FILE REFERENCE: 46143/294851
;  CURRENT APPLICATION NUMBER: US/11/177,506
;  CURRENT FILING DATE:  2005-07-08
;  PRIOR APPLICATION NUMBER: 60/586,856
;  PRIOR FILING DATE: 2004-07-09
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 1663
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-177-506-34

  Query Match             100.0%;  Score 91;  DB 11;  Length 1663;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 KNRWEDPGKQLYNVEA 16
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Db       1217 KNRWEDPGKQLYNVEA 1232


RESULT 6
US-10-514-462-11
; Sequence 11, Application US/10514462
; Publication No. US20060088909A1
; GENERAL INFORMATION:
;  APPLICANT: Emory University
;  TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic
;  TITLE OF INVENTION:  Compositions
;  FILE REFERENCE: 050508-2210
;  CURRENT APPLICATION NUMBER: US/10/514,462
;  CURRENT FILING DATE:  2004-11-12
;  PRIOR APPLICATION NUMBER: 60/381,557
;  PRIOR FILING DATE: 2002-05-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: C3d sequence
US-10-514-462-11

  Query Match             80.2%;  Score 73;  DB 8;  Length 300;
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  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              :||||:| :|||||||
Db        197 RNRWEEPDQQLYNVEA 212


RESULT 7
US-11-079-463-5775
; Sequence 5775, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: PATH00-03DIV2
;  CURRENT APPLICATION NUMBER: US/11/079,463
;  CURRENT FILING DATE:  2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/128,705
;  PRIOR FILING DATE: 1999-04-09
;  PRIOR APPLICATION NUMBER: US 09/540,209
;  PRIOR FILING DATE: 2000-04-04
;  NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 5775
;   LENGTH: 347
;   TYPE: PRT
;   ORGANISM: B.fragilis
US-11-079-463-5775

  Query Match             47.3%;  Score 43;  DB 11;  Length 347;
  Best Local Similarity   63.6%;  Pred. No. 14;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 WEDPGKQLYNV 14
              |||| ||| ::
Db        295 WEDPKKQLSDI 305


RESULT 8
US-10-514-055-5
; Sequence 5, Application US/10514055
; Publication No. US20060073576A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON CORPORATION
;  TITLE OF INVENTION: HIV ENVELOPE-CD4 COMPLEXES AND HYBRIDS
;  FILE REFERENCE: PP18701.003  (CHIR-18701/02WO)
;  CURRENT APPLICATION NUMBER: US/10/514,055
;  CURRENT FILING DATE:  2004-11-08
;  PRIOR APPLICATION NUMBER: 60/459,314
;  PRIOR FILING DATE: 2003-03-31
;  PRIOR APPLICATION NUMBER: 60/378,543
;  PRIOR FILING DATE: 2002-05-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 499
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: gp120.modSF62
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (127)..(151)
;   OTHER INFORMATION: V1 loop
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (152)..(191)
;   OTHER INFORMATION: V2 loop
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (291)..(324)
;   OTHER INFORMATION: V3 loop
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (378)..(405)
;   OTHER INFORMATION: V4 loop
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (447)..(459)
;   OTHER INFORMATION: V5 loop
US-10-514-055-5

  Query Match             47.3%;  Score 43;  DB 9;  Length 499;
  Best Local Similarity   54.5%;  Pred. No. 21;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              |||:: || :|
Db        412 NRWQEVGKAMY 422


RESULT 9
US-11-188-298-713
; Sequence 713, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53452)B
;  CURRENT APPLICATION NUMBER: US/11/188,298
;  CURRENT FILING DATE:  2005-07-22
;  PRIOR APPLICATION NUMBER: 60/592,978
;  PRIOR FILING DATE: 2004-07-31
;  NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 713
;   LENGTH: 591
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae TIGR4
US-11-188-298-713

  Query Match             47.3%;  Score 43;  DB 11;  Length 591;
  Best Local Similarity   46.7%;  Pred. No. 25;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVE 15
              ||::||  | |: |:
Db        475 KNKYEDTNKHLFGVD 489
```

```
RESULT 10
US-11-188-298-8505
; Sequence 8505, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53452)B
;  CURRENT APPLICATION NUMBER: US/11/188,298
;  CURRENT FILING DATE:  2005-07-22
;  PRIOR APPLICATION NUMBER: 60/592,978
;  PRIOR FILING DATE: 2004-07-31
;  NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 8505
;   LENGTH: 591
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae R6
US-11-188-298-8505

  Query Match             47.3%;  Score 43;  DB 11;  Length 591;
  Best Local Similarity   46.7%;  Pred. No. 25;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVE 15
              ||::||  | |: |:
Db        475 KNKYEDTNKHLFGVD 489


RESULT 11
US-11-188-298-10639
; Sequence 10639, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53452)B
;  CURRENT APPLICATION NUMBER: US/11/188,298
;  CURRENT FILING DATE:  2005-07-22
;  PRIOR APPLICATION NUMBER: 60/592,978
;  PRIOR FILING DATE: 2004-07-31
;  NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 10639
;   LENGTH: 591
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-11-188-298-10639

  Query Match             47.3%;  Score 43;  DB 11;  Length 591;
  Best Local Similarity   46.7%;  Pred. No. 25;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVE 15
              ||::||  | |: |:
Db        475 KNKYEDTNKHLFGVD 489


RESULT 12
US-11-188-298-13585
; Sequence 13585, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53452)B
;  CURRENT APPLICATION NUMBER: US/11/188,298
;  CURRENT FILING DATE:  2005-07-22
;  PRIOR APPLICATION NUMBER: 60/592,978
;  PRIOR FILING DATE: 2004-07-31
;  NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 13585
;   LENGTH: 591
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-11-188-298-13585

  Query Match             47.3%;  Score 43;  DB 11;  Length 591;
  Best Local Similarity   46.7%;  Pred. No. 25;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVE 15
              ||::||  | |: |:
Db        475 KNKYEDTNKHLFGVD 489


RESULT 13
US-11-188-298-1487
; Sequence 1487, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-21(53452)B
;  CURRENT APPLICATION NUMBER: US/11/188,298
;  CURRENT FILING DATE:  2005-07-22
;  PRIOR APPLICATION NUMBER: 60/592,978
;  PRIOR FILING DATE: 2004-07-31
;  NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 1487
;   LENGTH: 655
;   TYPE: PRT
;   ORGANISM: Clostridium tetani E88
US-11-188-298-1487

  Query Match             47.3%;  Score 43;  DB 11;  Length 655;
  Best Local Similarity   46.7%;  Pred. No. 27;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVE 15
              || ||    :|:|:|
Db        385 KNEWEKELNRLFNIE 399


RESULT 14
US-11-100-356-2
; Sequence 2, Application US/11100356
; Publication No. US20060057115A1
; GENERAL INFORMATION:
;  APPLICANT: ZUR MEGEDE, Jan
;  APPLICANT:  BARNETT, Susan
;  APPLICANT:  LIAN, Ying
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
;  TITLE OF INVENTION:  POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
;  FILE REFERENCE: 2300-1621.20
;  CURRENT APPLICATION NUMBER: US/11/100,356
;  CURRENT FILING DATE:  2005-04-06
;  PRIOR APPLICATION NUMBER: US/10/190,434
;  PRIOR FILING DATE: 2002-07-05
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 842
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: SF162
US-11-100-356-2

  Query Match             47.3%;  Score 43;  DB 11;  Length 842;
  Best Local Similarity   54.5%;  Pred. No. 35;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              |||:: || :|
Db        410 NRWQEVGKAMY 420
```

```
RESULT 15
US-10-514-462-1
; Sequence 1, Application US/10514462
; Publication No. US20060088909A1
; GENERAL INFORMATION:
;  APPLICANT: Emory University
;  TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic
;  TITLE OF INVENTION:  Compositions
;  FILE REFERENCE: 050508-2210
;  CURRENT APPLICATION NUMBER: US/10/514,462
;  CURRENT FILING DATE:  2004-11-12
;  PRIOR APPLICATION NUMBER: 60/381,557
;  PRIOR FILING DATE: 2002-05-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 847
;   TYPE: PRT
;   ORGANISM: HIV SF162 Envelope Protein
US-10-514-462-1

  Query Match             47.3%;  Score 43;  DB 8;  Length 847;
  Best Local Similarity   54.5%;  Pred. No. 36;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              |||:: || :|
Db        415 NRWQEVGKAMY 425


Search completed: May 15, 2006, 16:35:07
Job time : 29 secs
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GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 15, 2006, 16:12:36 ; Search time 38 Seconds
(without alignments)
40.512 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	100.0	1663	1	C3HU	complement C3 prec
2	80	87.9	1663	1	C3RT	complement C3 prec
3	79	86.8	726	2	A27602	complement C3 - ra
4	73	80.2	1663	1	C3MS	complement C3 prec
5	58	63.7	1666	1	C3GP	complement C3 prec
6	52	57.1	1358	2	B86241	hypothetical prote
7	44.5	48.9	490	2	D71401	probable selenium-
8	44	48.4	590	2	A44068	cell pattern forma
9	43	47.3	78	2	G82153	hypothetical prote
10	43	47.3	432	2	T05236	hypothetical prote
11	43	47.3	591	2	B97952	pyruvate oxidase (
12	43	47.3	591	2	F95084	pyruvate oxidase [
13	43	47.3	852	2	T12016	envelope glycoprot
14	43	47.3	1651	1	C3NJ	complement C3 prec
15	42.5	46.7	537	2	B90598	ABC transporter at
16	42	46.2	923	2	E83574	hypothetical prote
17	41	45.1	359	2	S45700	G-alpha-11 protein
18	41	45.1	538	2	E85438	step II splicing f
19	41	45.1	574	2	T16230	hypothetical prote
20	41	45.1	2166	2	G70163	hypothetical prote
21	41	45.1	5138	2	B96695	hypothetical prote
22	40.5	44.5	400	1	JC1428	ketol-acid reducto
23	40	44.0	166	2	A85077	hypothetical prote
24	40	44.0	274	2	S75320	hypothetical prote
25	40	44.0	290	2	G82360	diaminopimelate ep
26	40	44.0	311	2	C89894	methionyl-tRNA for
27	40	44.0	331	2	AI2972	two component sens
28	40	44.0	331	2	B98310	probable transmemb
29	40	44.0	359	1	RGHUGY	GTP-binding regula
30	40	44.0	432	2	B96515	hypothetical prote
31	40	44.0	434	2	C96515	hypothetical prote
32	40	44.0	630	2	JQ1670	polygalacturonase
33	40	44.0	647	2	G70733	probable htpG prot
34	40	44.0	1320	2	E59092	hypothetical prote
35	39.5	43.4	447	2	T07705	hypothetical prote
36	39	42.9	274	2	AE0468	diaminopimelate ep
37	39	42.9	302	2	H86271	protein F16A14.8 [
38	39	42.9	357	2	AF2796	lipoprotein [impor
39	39	42.9	363	2	AE3597	ABC transporter pe
40	39	42.9	364	2	D95364	hypothetical prote
41	39	42.9	371	2	F97575	hypothetical prote
42	39	42.9	400	2	AI0104	probable galactosi
43	39	42.9	427	2	JC4565	chitinase (EC 3.2.
44	39	42.9	428	2	T08576	phenylalanine-tRNA
45	39	42.9	606	2	G72282	hypothetical prote

ALIGNMENTS

RESULT 1
C3HU
complement C3 precursor [validated] - human
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C;Accession: A94065; A37999; A92187; A27603; A23435; A45830; B45830; A01257; A01258
R;de Bruijn, M.H.L.; Fey, G.H.
Proc. Natl. Acad. Sci. U.S.A. 82, 708-712, 1985
A;Title: Human complement component C3: cDNA coding sequence and derived primary struct
A;Reference number: A94065; MUID:85140166; PMID:2579379
A;Accession: A94065
A;Molecule type: mRNA
A;Residues: 1-1663 <DEB>
A;Cross-references: UNIPROT:P01024; UNIPARC:UPI0000047168; GB:K02765; NID:g179664; PIDN
R;Vik, D.P.; Amiguet, P.; Moffat, G.J.; Fey, M.; Amiguet-Barras, F.; Wetsel, R.A.; Tack,
Biochemistry 30, 1080-1085, 1991
A;Title: Structural features of the human C3 gene: intron/exon organization, transcript
A;Reference number: A37999; MUID:91113687; PMID:1703437
A;Contents: intron/exon structure of gene
A;Accession: A37999
A;Molecule type: DNA
A;Residues: 1-25 <VIK>
A;Cross-references: UNIPARC:UPI0000173214; GB:M63423
A;Note: the authors translated the codon GGT for residue 6 as Leu, CCC for residue 7 as
R;Hugli, T.E.
J. Biol. Chem. 250, 8293-8301, 1975
A;Title: Human anaphylatoxin (C3a) from the third component of complement.
A;Reference number: A92187; MUID:76069169; PMID:1238393
A;Accession: A92187
A;Molecule type: protein
A;Residues: 672-680,'N',682-699,'Q',701-748 <HUG>
A;Cross-references: UNIPARC:UPI0000150417
R;Daoudaki, M.E.; Becherer, J.D.; Lambris, J.D.
J. Immunol. 140, 1577-1580, 1988
A;Title: A 34-amino acid peptide of the third component of complement mediates properdi
A;Reference number: A27603; MUID:88154452; PMID:3279119
A;Accession: A27603
A;Molecule type: protein
A;Residues: 1409-1563 <DAO>
A;Cross-references: UNIPARC:UPI0000173215
R;Hellman, U.; Eggertsen, G.; Engstrom, A.; Sjoquist, J.
Biochem. J. 230, 353-361, 1985
A;Title: Amino acid sequence of the trypsin-generated C3d fragment from human complemen
A;Reference number: A23435; MUID:86025442; PMID:3876831
A;Accession: A23435
A;Molecule type: protein
A;Residues: 1002-1012,'E',1014-1303 <HEL>
A;Cross-references: UNIPARC:UPI0000173216
A;Note: sequence corresponding to residues 1072-1100 was not determined but was taken f
R;Poznansky, M.C.; Clissold, P.M.; Lachmann, P.J.
J. Immunol. 143, 1254-1258, 1989

A;Title: The difference between human C3F and C3S results from a single amino acid chang
3.
A;Reference number: A45830; MUID:89309808; PMID:2473125
A;Accession: A45830
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1212-1215,'N',1217-1223 <POZ>
A;Cross-references: UNIPARC:UPI0000173217
A;Note: this is the C3S allele
A;Accession: B45830
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1212-1223 <PO2>
A;Cross-references: UNIPARC:UPI0000173218
R;Dolmer, K.; Sottrup-Jensen, L.
FEBS Lett. 315, 85-90, 1993
A;Title: Disulfide bridges in human complement component C3b.
A;Reference number: S27041; MUID:93106233; PMID:8416818
A;Contents: annotation; disulfide bonds
C;Comment: The sequence shown is the C3 fast (C3F) allele, which is found mainly in Cauc
C;Comment: Complement C3 contains two chains, formed by removal of four residues and lin
 alternative complement pathways, releases the C3a anaphylatoxin from the amino end of t
rnative-complement-pathway C3/C5 convertase.
C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign pa
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pro
C;Comment: The major site of synthesis of this plasma protein is the liver.
C;Genetics:
A;Gene: GDB:C3
A;Cross-references: GDB:119044; OMIM:120700
A;Map position: 19p13.3-19p13.3
A;Note: contains 41 exons
C;Superfamily: alpha-2-macroglobulin
C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein;
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-667/Product: complement C3 and C3b beta chain #status predicted <C3BB>
F;23-667,672-1663/Product: complement C3 #status predicted <CC3>
F;23-667,749-1663/Product: C3b #status predicted <C3B>
F;672-1663/Product: complement C3 alpha chain #status predicted <CC3A>
F;672-748/Product: C3a anaphylatoxin #status predicted <C3T>
F;749-1663/Product: C3b alpha' chain #status predicted <C3BA>
F;946-1303/Product: C3dk fragment #status predicted <CDK>
F;955-1303/Product: C3dg fragment #status predicted <CDG>
F;955-1001/Product: C3g fragment #status predicted <C3G>
F;1002-1303/Product: C3d fragment #status experimental <C3D>
F;1424-1457/Region: properdin binding
F;85,939/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;559-816,627-662,693-720,694-727,707-728,873-1513,1101-1158,1358-1489,1389-1458,1506-15
F;748-749/Cleavage site: Arg-Ser (C3 convertase) #status predicted
F;954-955/Cleavage site: Arg-Glu (complement factor I) #status predicted
F;1010-1013/Cross-link: thiolester (Cys-Gln) #status experimental
F;1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted
F;1320-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted
F;1617/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match 100.0%; Score 91; DB 1; Length 1663;
  Best Local Similarity 100.0%; Pred. No. 2e-06;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
||||||||||||||||
Db 1217 KNRWEDPGKQLYNVEA 1232

RESULT 2
C3RT
complement C3 precursor - rat
N;Alternate names: 37K phospholipase A2 inhibitory protein
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1992 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: S15764; A54562; A01260; B35979; A35979; PN0567; PN0566; A32281; S08692
R;Misumi, Y.; Sohda, M.; Ikehara, Y.
Nucleic Acids Res. 18, 2178, 1990
A;Title: Nucleotide and deduced amino acid sequence of rat complement C3.
A;Reference number: S15764; MUID:90245672; PMID:2336397
A;Accession: S15764
A;Molecule type: mRNA
A;Residues: 1-1663 <MIS>
A;Cross-references: UNIPROT:P01026; UNIPARC:UPI0000127C4E; EMBL:X52477; NID:g56953; PID
R;Sundstrom, S.A.; Komm, B.S.; Ponce-de-Leon, H.; Yi, Z.; Teuscher, C.; Lyttle, C.R.
J. Biol. Chem. 264, 16941-16947, 1989
A;Title: Estrogen regulation of tissue-specific expression of complement C3.
A;Reference number: A54562; MUID:89380332; PMID:2674144
A;Accession: A54562
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 'P',1316-1595 <SUN>
A;Cross-references: UNIPARC:UPI00001708A4; GB:M29866; NID:g203200; PIDN:AAA40837.1; PID
R;Jacobs, J.W.; Rubin, J.S.; Hugli, T.E.; Bogardt, R.A.; Mariz, I.K.; Daniels, J.S.; Da
Biochemistry 17, 5031-5038, 1978
A;Title: Purification, characterization, and amino acid sequence of rat anaphylatoxin (
A;Reference number: A01260; MUID:79062262; PMID:309768
A;Accession: A01260
A;Molecule type: protein
A;Residues: 671-703,'K',705-720,'KL',723-748 <JAC>
A;Cross-references: UNIPARC:UPI0000150418
A;Note: three disulfide bonds are present
R;Suwa, Y.; Kudo, I.; Imaizumi, A.; Okada, M.; Kamimura, T.; Suzuki, Y.; Chang, H.W.; Ha
Proc. Natl. Acad. Sci. U.S.A. 87, 2395-2399, 1990
A;Title: Proteinaceous inhibitors of phospholipase A-2 purified from inflammatory sites
A;Reference number: A35979; MUID:90207203; PMID:2320562
A;Accession: B35979
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'X',998-1005 <SUW>
A;Cross-references: UNIPARC:UPI0000173221
A;Accession: A35979
A;Molecule type: protein
A;Residues: 'X',961-962,'P',964-969 <SU2>
A;Cross-references: UNIPARC:UPI0000173221
R;Nakagawa, H.; Komorita, N.
Biochem. Biophys. Res. Commun. 194, 1181-1187, 1993
A;Title: Complement component C3-derived neutrophil chemotactic factors purified from e
A;Reference number: PN0566; MUID:93356786; PMID:8352775
A;Accession: PN0567
A;Molecule type: protein
A;Residues: 568-592 <NAK>
A;Cross-references: UNIPARC:UPI00000E621C
A;Note: amino end of a C3-derived peptide designated exudate neutrophil chemotactic fac
A;Accession: PN0566
A;Molecule type: protein
A;Residues: 671-687 <NA2>
A;Cross-references: UNIPARC:UPI00000E8594
A;Note: amino end of peptide designated neutrophil chemotactic factor 1 and probably id
R;Kuivanen, P.C.; Capulong, R.B.; Harkins, R.N.; DeSombre, E.R.
Biochem. Biophys. Res. Commun. 158, 898-905, 1989
A;Title: The estrogen-responsive 110K and 74K rat uterine secretory proteins are struct
A;Reference number: A32281; MUID:89149812; PMID:2645873
A;Accession: A32281
A;Molecule type: protein
A;Residues: 25-41 <KUI>
A;Cross-references: UNIPARC:UPI0000173223
A;Experimental source: 17beta-estradiol-stimulated uterus of immature rat
A;Note: the authors treat this 74K uterine secretory protein, identical as far as seque
ent
C;Comment: Complement C3 contains two chains, formed by removal of four residues and li
 alternative complement pathways, releases the C3a anaphylatoxin from the amino end of
rnative-complement-pathway C3/C5 convertase.
C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign p
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pr
C;Comment: The major site of synthesis of this plasma protein is the liver.
C;Superfamily: alpha-2-macroglobulin
C;Keywords: acute phase; chemotaxis; complement alternate pathway; complement pathway;
F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-666/Product: complement C3 and C3b beta chain #status predicted <C3BB>
F;25-666,671-1663/Product: complement C3 #status predicted <CC3>
F;25-666,749-1663/Product: complement C3b #status predicted <C3B>
F;671-1663/Product: complement C3 alpha chain #status predicted <CC3A>
F;671-748/Product: C3a anaphylatoxin #status experimental <C3T>
F;749-1663/Product: complement C3b alpha' chain #status predicted <C3BA>
F;946-1303/Product: C3dk fragment #status predicted <CDK>
F;1002-1303/Product: C3d fragment #status predicted <C3D>
F;1424-1457/Region: properdin binding
F;558-816,626-661,693-720,694-727,707-728,873-1513,1101-1158,1358-1489,1389-1458,1506-15
F;748-749/Cleavage site: Arg-Ser (C3 convertase) #status predicted
F;939,1617/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1010-1013/Cross-link: thiolester (Cys-Gln) #status predicted
F;1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted
F;1320-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted

  Query Match 87.9%; Score 80; DB 1; Length 1663;
  Best Local Similarity 81.2%; Pred. No. 0.00012;
  Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
:||||:||:|||||||
Db 1217 RNRWEEPGQQLYNVEA 1232

RESULT 3
A27602
complement C3 - rabbit (fragment)
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 15-Dec-1988 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: A27602
R;Kusano, M.; Choi, N.H.; Tomita, M.; Yamamoto, K.; Migita, S.; Sekiya, T.; Nishimura, S
Immunol. Invest. 15, 365-378, 1986
A;Title: Nucleotide sequence of cDNA and derived amino acid sequence of rabbit complemen
A;Reference number: A27602; MUID:87006907; PMID:3019881
A;Accession: A27602
A;Molecule type: mRNA
A;Residues: 1-726 <KUS>
A;Cross-references: UNIPROT:P12247; UNIPARC:UPI0000127C4D; GB:M32434; NID:g164862; PIDN:
C;Comment: Complement C3 contains two chains, formed by removal of four residues and lin
alternative complement pathways, releases the C3a anaphylatoxin from the amino end of t
rnative-complement-pathway C3/C5 convertase.
C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign pa
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pro
C;Comment: The major site of synthesis of this plasma protein is the liver.
C;Superfamily: alpha-2-macroglobulin
C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein;

  Query Match 86.8%; Score 79; DB 2; Length 726;
  Best Local Similarity 81.2%; Pred. No. 7.5e-05;
  Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
|||||:||::||||||
Db 280 KNRWEEPGQRLYNVEA 295

RESULT 4
C3MS
complement C3 precursor - mouse
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A92459; B92459; A92460; A93938; A21898; A54561; S16369; S16189; I49563; I49
R;Lundwall, A.; Wetsel, R.A.; Domdey, H.; Tack, B.F.; Fey, G.H.
J. Biol. Chem. 259, 13851-13856, 1984
A;Title: Structure of murine complement component C3: I. Nucleotide sequence of cloned c
A;Reference number: A92459; MUID:85054818; PMID:6548745
A;Accession: A92459
A;Molecule type: mRNA
A;Residues: 1-724 <LU1>
A;Cross-references: UNIPROT:P01027; UNIPARC:UPI0000173219
A;Accession: B92459
A;Molecule type: DNA
A;Residues: 1-124 <LU2>
A;Cross-references: UNIPARC:UPI000017321A
R;Wetsel, R.A.; Lundwall, A.; Davidson, F.; Gibson, T.; Tack, B.F.; Fey, G.H.
J. Biol. Chem. 259, 13857-13862, 1984
A;Title: Structure of murine complement component C3: II. Nucleotide sequence of cloned
A;Reference number: A92460; MUID:85054819; PMID:6094532
A;Accession: A92460
A;Molecule type: mRNA
A;Residues: 671-1663 <WET>
A;Cross-references: UNIPARC:UPI000017321B
R;Domdey, H.; Wiebauer, K.; Kazmaier, M.; Muller, V.; Odink, K.; Fey, G.
Proc. Natl. Acad. Sci. U.S.A. 79, 7619-7623, 1982
A;Title: Characterization of the mRNA and cloned cDNA specifying the third component of
A;Reference number: A93938; MUID:83117730; PMID:6961437
A;Contents: C3a
A;Accession: A93938
A;Molecule type: mRNA
A;Residues: 671-748 <DOM>
A;Cross-references: UNIPARC:UPI0000150419
R;Sottrup-Jensen, L.; Stepanik, T.M.; Kristensen, T.; Lonblad, P.B.; Jones, C.M.; Wierzb
Proc. Natl. Acad. Sci. U.S.A. 82, 9-13, 1985
A;Title: Common evolutionary origin of alpha2-macroglobulin and complement components C3
A;Reference number: A21898; MUID:85113177; PMID:2578664
A;Accession: A21898
A;Molecule type: mRNA
A;Residues: 25-1663 <SOT>
A;Cross-references: UNIPARC:UPI000017321C
R;Hamada, J.; Cavanaugh, P.G.; Miki, K.; Nicolson, G.L.
Cancer Res. 53, 4418-4423, 1993
A;Title: A paracrine migration-stimulating factor for metastatic tumor cells secreted by
A;Reference number: A54561; MUID:93373334; PMID:8364938
A;Accession: A54561
A;Molecule type: protein
A;Residues: 25-41;749-760 <HAM>
A;Cross-references: UNIPARC:UPI000017321D; UNIPARC:UPI000017321E
A;Experimental source: migration-stimulating factor purified from medium conditioned by
R;Sato, T.; Hong, M.H.; Jin, C.H.; Ishimi, Y.; Udagawa, N.; Shinki, T.; Abe, E.; Suda,
FEBS Lett. 285, 21-24, 1991
A;Title: The specific production of the third component of complement by osteoblastic c
A;Reference number: S16189; MUID:91293304; PMID:2065778
A;Accession: S16369
A;Molecule type: protein
A;Residues: 25-31 <SAT>
A;Cross-references: UNIPARC:UPI000017321F
A;Accession: S16189
A;Status: preliminary
A;Molecule type: protein
A;Residues: 671-677,'X',679-680 <SA2>
A;Cross-references: UNIPARC:UPI000017321F
R;Fey, G.; Domdey, H.; Wiebauer, K.; Whitehead, A.S.; Odink, K.
Springer Semin. Immunopathol. 6, 119-147, 1983
A;Title: Structure and expression of the C3 gene.
A;Reference number: I49563; MUID:84045280; PMID:6356427
A;Accession: I49563
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 25-136,'Q',138-240 <FEY>
A;Cross-references: UNIPARC:UPI00000E6D15; GB:M35659; NID:g192280; PIDN:AAA37339.1; PID
R;Fey, G.H.; Wiebauer, K.; Domdey, H.
Ann. N. Y. Acad. Sci. 421, 307-312, 1983
A;Title: Amino acid sequences of mouse complement C3 derived from nucleotide sequences
A;Reference number: I49576; MUID:84201365; PMID:6609661
A;Accession: I49576
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 658-761 <RES>
A;Cross-references: UNIPARC:UPI000016CC86; GB:M33032; NID:g192391; PIDN:AAA37378.1; PID
C;Comment: Complement C3 contains two chains, formed by removal of four residues and li
alternative complement pathways, releases the C3a anaphylatoxin from the amino end of
rnative-complement-pathway C3/C5 convertase.

C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign pa
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pro
C;Comment: The major site of synthesis of this plasma protein is the liver.
C;Genetics:
A;Introns: 27/2; 90/3
A;Note: the list of introns may be incomplete
C;Superfamily: alpha-2-macroglobulin
C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein;
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-666/Product: complement C3 and C3b beta chain #status predicted <C3BB>
F;25-666,671-1663/Product: complement C3 #status predicted <CC3>
F;25-666,749-1663/Product: C3b #status predicted <C3B>
F;671-1663/Product: complement C3 alpha chain #status predicted <CC3A>
F;671-748/Product: C3a anaphylatoxin #status predicted <C3T>
F;749-1663/Product: C3b alpha' chain #status predicted <C3BA>
F;946-1303/Product: C3dk fragment #status predicted <CDK>
F;1002-1303/Product: C3d fragment #status predicted <C3D>
F;1424-1457/Region: properdin binding
F;559-816,626-661,693-720,694-727,707-728,873-1513,1101-1158,1358-1489,1389-1458,1506-15
F;748-749/Cleavage site: Arg-Ser (C3 convertase) #status predicted
F;939,1617/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1010-1013/Cross-link: thiolester (Cys-Gln) #status predicted
F;1303-1304/Cleavage site: Arg-Ser (complement factor I) #status predicted
F;1320-1321/Cleavage site: Arg-Ser (complement factor I) #status predicted

  Query Match 80.2%; Score 73; DB 1; Length 1663;
  Best Local Similarity 75.0%; Pred. No. 0.0017;
  Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
:||||:| :|||||||
Db 1217 RNRWEEPDQQLYNVEA 1232

RESULT 5
C3GP
complement C3 precursor - guinea pig
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-Feb-1992 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: A37156; S03375; A20342; D20342; C20342; A31222
R;Auerbach, H.S.; Burger, R.; Dodds, A.; Colten, H.R.
J. Clin. Invest. 86, 96-106, 1990
A;Title: Molecular basis of complement C3 deficiency in guinea pigs.
A;Reference number: A37156; MUID:90307998; PMID:1973176
A;Accession: A37156
A;Molecule type: mRNA
A;Residues: 1-1666 <AUE>
A;Cross-references: UNIPROT:P12387; UNIPARC:UPI0000127C48; GB:M34054; NID:g191262; PIDN:
R;Gerard, N.P.; Lively, M.O.; Gerard, C.
Protein Seq. Data Anal. 1, 473-478, 1988
A;Title: Amino acid sequence of guinea pig C3a anaphylatoxin.
A;Reference number: S03375; MUID:89113342; PMID:3064079
A;Accession: S03375
A;Molecule type: protein
A;Residues: 676-730,'N',732-752 <GER>
A;Cross-references: UNIPARC:UPI0000173224
A;Experimental source: complement-activated guinea pig serum
A;Note: form isolated is inactive C3a anaphylatoxin and is missing the carboxyl-terminal
R;Thomas, M.L.; Tack, B.F.
Biochemistry 22, 942-947, 1983
A;Title: Identification and alignment of a thiol ester site in the third component of gu
A;Reference number: A90479; MUID:83178889; PMID:6838833
A;Accession: A20342
A;Molecule type: protein
A;Residues: 676-687 <TH1>
A;Cross-references: UNIPARC:UPI0000173225
A;Accession: D20342
A;Molecule type: protein
A;Residues: 993-1012,1014-1017,'E',1019-1030,'Y' <TH2>
A;Cross-references: UNIPARC:UPI0000173225
R;Goldberger, G.; Thomas, M.L.; Tack, B.F.; Williams, J.; Colten, H.R.; Abraham, G.N.
J. Biol. Chem. 256, 12617-12619, 1981
A;Title: NH2-terminal structure and cleavage of guinea pig pro-C3, the precursor of the
A;Reference number: A20342; MUID:82075767; PMID:6458605
A;Accession: C20342
A;Molecule type: protein
A;Residues: 23-38 <GOL>
A;Cross-references: UNIPARC:UPI0000173227
C;Comment: Complement C3 contains two chains, formed by removal of four residues and li
alternative complement pathways, releases the C3a anaphylatoxin from the amino end of
rnative-complement-pathway C3/C5 convertase.
C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign p
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pr
C;Comment: The major site of synthesis of this plasma protein is the liver.
C;Superfamily: alpha-2-macroglobulin
C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein,
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-671/Product: complement C3 and C3b beta chain #status predicted <C3BB>
F;23-671,676-1666/Product: complement C3 #status predicted <CC3>
F;23-671,754-1666/Product: complement C3b #status predicted <C3B>
F;676-1666/Product: complement C3 alpha chain #status predicted <CC3A>
F;676-753/Product: C3a anaphylatoxin #status predicted <C3T>
F;754-1666/Product: complement C3b alpha' chain #status predicted <C3BA>
F;951-1308/Product: C3dk fragment #status predicted <CDK>
F;1007-1308/Product: C3d fragment #status predicted <C3D>
F;1429-1461/Region: properdin binding
F;557-821,630-666,698-725,699-732,712-733,878-1517,1106-1163,1363-1493,1394-1462,1510-1
F;753-754/Cleavage site: Arg-Ser (C3 convertase) #status predicted
F;944,1620/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1015-1018/Cross-link: thiolester (Cys-Gln) #status experimental
F;1308-1309/Cleavage site: Arg-Ser (complement factor I) #status predicted
F;1325-1326/Cleavage site: Arg-Ser (complement factor I) #status predicted

  Query Match 63.7%; Score 58; DB 1; Length 1666;
  Best Local Similarity 62.5%; Pred. No. 0.5;
  Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
|||||: ::||:|||
Db 1222 KNRWEEARQKLYSVEA 1237

RESULT 6
B86241
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86241
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B86241
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1358 <STO>
A;Cross-references: UNIPROT:Q9SAC6; UNIPARC:UPI00000A10C3; GB:AE005172; NID:g4874272; P
C;Genetics:
A;Map position: 1

  Query Match 57.1%; Score 52; DB 2; Length 1358;
  Best Local Similarity 69.2%; Pred. No. 3.9;
  Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RWEDPGKQLYNVE 15
||| |||:|| |

```
Db        223 RWERKGKQMYNPE 235


RESULT 7
D71401
probable selenium-binding protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession: D71401
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
 P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: D71401
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-490 <BEV>
A;Cross-references: UNIPROT:O23264; UNIPARC:UPI0000000E71; GB:Z97335; NID:g2244747; PID:
C;Genetics:
A;Map position: 4COP9-4G3845
C;Superfamily: Caenorhabditis elegans hypothetical protein Y37A1B.5

  Query Match             48.9%;  Score 44.5;  DB 2;  Length 490;
  Best Local Similarity   56.2%;  Pred. No. 22;
  Matches    9;  Conservative    1;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 KNRWEDPG-KQLYNVE 15
              ||||| ||   ||  :
Db        191 KNRWEKPGHSPLYGYD 206


RESULT 8
A44068
cell pattern formation-associated protein - Emericella nidulans
N;Alternate names: cell differentiation and spatial organization regulator stuA
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44068; S27413
R;Miller, K.Y.; Wu, J.; Miller, B.L.
Genes Dev. 6, 1770-1782, 1992
A;Title: StuA is required for cell pattern formation in Aspergillus.
A;Reference number: A44068; MUID:92387550; PMID:1516832
A;Accession: A44068
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-590 <MIL>
A;Cross-references: UNIPROT:P36011; UNIPARC:UPI0000136159; EMBL:M83569; NID:g168095; PID
A;Note: sequence extracted from NCBI backbone (NCBIP:112625)
C;Genetics:
A;Introns: 92/1; 157/1; 201/2
C;Keywords: DNA binding; nucleus; transcription regulation

  Query Match             48.4%;  Score 44;  DB 2;  Length 590;
  Best Local Similarity   61.5%;  Pred. No. 32;
  Matches    8;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 WEDPGKQLYNVEA 16
              ||| |   | |||
Db        135 WEDEGSLCYQVEA 147


RESULT 9
G82153
hypothetical protein VC1802 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82153
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.,
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82153
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-78 <HEI>
A;Cross-references: UNIPROT:Q9KR44; UNIPARC:UPI00000C30F3; GB:AE004257; GB:AE003852; NI
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1802
A;Map position: 1

  Query Match             47.3%;  Score 43;  DB 2;  Length 78;
  Best Local Similarity   87.5%;  Pred. No. 5.4;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 DPGKQLYN 13
              ||||:|||
Db         11 DPGKELYN 18


RESULT 10
T05236
hypothetical protein F18A5.60 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05236
R;Bevan, M.; Weber, N.; Grueninger, D.; Schmidheini, T.; Bancroft, I.; Mewes, H.W.; May
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15405
A;Accession: T05236
A;Molecule type: DNA
A;Residues: 1-432 <BEV>
A;Cross-references: UNIPROT:Q9SVP5; UNIPARC:UPI00000A22A3; EMBL:AL035528
A;Experimental source: cultivar Columbia; BAC clone F18A5
C;Genetics:
A;Map position: 4
A;Introns: 191/3; 223/3; 274/2; 389/1; 401/3
A;Note: F18A5.60

  Query Match             47.3%;  Score 43;  DB 2;  Length 432;
  Best Local Similarity   66.7%;  Pred. No. 34;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGK 9
              :||||| :
Db        348 ENRWEDPSR 356


RESULT 11
B97952
pyruvate oxidase (EC 1.2.3.3) [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 31-Dec-2004
C;Accession: B97952
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B97952
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-591 <KUR>
A;Cross-references: UNIPROT:Q8DQJ4; UNIPARC:UPI00000E34BC; GB:AE007317; PIDN:AAK99446.1
C;Genetics:
A;Gene: spxB
```

```
C;Superfamily: thiamine diphosphate-dependent enzyme, acetolactate synthase type
C;Keywords: oxidoreductase

  Query Match             47.3%;  Score 43;  DB 2;  Length 591;
  Best Local Similarity   46.7%;  Pred. No. 47;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVE 15
              ||::||  | |: |:
Db        475 KNKYEDTNKHLFGVD 489


RESULT 12
F95084
pyruvate oxidase [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 31-Dec-2004
C;Accession: F95084
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: F95084
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-591 <KUR>
A;Cross-references: UNIPROT:Q54970; UNIPARC:UPI000005156C; GB:AE005672; PIDN:AAK74871.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0730
C;Superfamily: thiamine diphosphate-dependent enzyme, acetolactate synthase type

  Query Match             47.3%;  Score 43;  DB 2;  Length 591;
  Best Local Similarity   46.7%;  Pred. No. 47;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVE 15
              ||::||  | |: |:
Db        475 KNKYEDTNKHLFGVD 489


RESULT 13
T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12016
R;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
A;Reference number: Z17379; MUID:98178716; PMID:9519894
A;Accession: T12016
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-852 <MCC>
A;Cross-references: UNIPROT:O41883; UNIPARC:UPI000010B1F2; EMBL:U90934; NID:g2351783; PI
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein

  Query Match             47.3%;  Score 43;  DB 2;  Length 852;
  Best Local Similarity   54.5%;  Pred. No. 70;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              |||:: || :|
Db        421 NRWQEVGKAMY 431


RESULT 14
C3NJ
complement C3 precursor - monocled cobra
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
C;Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)
C;Date: 18-Jun-1993 #sequence_revision 07-Oct-1994 #text_change 17-Mar-2000
C;Accession: A46513
R;Fritzinger, D.C.; Petrella, E.C.; Connelly, M.B.; Bredehorst, R.; Vogel, C.W.
J. Immunol. 149, 3554-3562, 1992
A;Title: Primary structure of cobra complement component C3.
A;Reference number: A46513; MUID:93056528; PMID:1431125
A;Accession: A46513
A;Molecule type: mRNA
A;Residues: 1-1651 <FRI>
A;Cross-references: UNIPARC:UPI0000127C4B; GB:L02365; NID:g213372; PIDN:AAA49385.1; PID
A;Note: authors' translation shows Arg-1408 after residue 1438 and, consequently, resid
A;Note: sequence extracted from NCBI backbone (NCBIP:118403) and corrected to correspon
C;Comment: Complement C3 contains two chains, formed by removal of four residues and li
 alternative complement pathways, releases the C3a anaphylatoxin from the amino end of
rnative-complement-pathway C3/C5 convertase.
C;Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
C;Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign p
e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pr
C;Comment: The major site of synthesis of this plasma protein is the liver.
C;Superfamily: alpha-2-macroglobulin
C;Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-655/Product: complement C3 and C3b beta chain #status predicted <C3BB>
F;23-655,660-1651/Product: complement C3 #status predicted <CC3>
F;23-655,739-1651/Product: complement C3b #status predicted <C3B>
F;660-1651/Product: complement C3 alpha chain #status predicted <CC3A>
F;660-738/Product: C3a anaphylatoxin #status predicted <C3T>
F;739-1651/Product: complement C3b alpha' chain #status predicted <C3BA>
F;1412-1445/Region: properdin binding
F;546-807,615-650,683-710,684-717,697-718,863-1501,1091-1147,1346-1477,1377-1446,1494-1
F;738-739/Cleavage site: Arg-Ser (C3 convertase) #status predicted
F;999-1002/Cross-link: thiolester (Cys-Gln) #status predicted

  Query Match             47.3%;  Score 43;  DB 1;  Length 1651;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVE 15
              :||||:   : :|:|
Db       1204 RNRWEEYNARTHNIE 1218


RESULT 15
B90598
ABC transporter atp-binding protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 05-Oct-2004
C;Accession: B90598
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: B90598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-537 <KUR>
A;Cross-references: UNIPROT:Q98PN2; UNIPARC:UPI00000D4649; GB:AL445566; PID:g14090105;
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU_6900
A;Genetic code: SGC3

  Query Match             46.7%;  Score 42.5;  DB 2;  Length 537;
  Best Local Similarity   56.2%;  Pred. No. 52;
  Matches    9;  Conservative    2;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          3 RWE---DPGKQLYNVE 15
              :||    |||| ||| 
Db        308 KWEINRVPGKQILNVE 323
```

Search completed: May 15, 2006, 16:16:59
Job time : 40 secs

GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 15, 2006, 16:08:46 ; Search time 185 Seconds
(without alignments)
38.000 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	100.0	16	4	AAB92360	Aab92360 Miscellan
2	91	100.0	16	6	ABP58217	Abp58217 Immunosti
3	91	100.0	16	8	ADS17594	Ads17594 Peptide d
4	91	100.0	16	9	ADV24825	Adv24825 CR2-bindi
5	91	100.0	17	9	ADV24829	Adv24829 Complemen
6	91	100.0	17	9	ADV24828	Adv24828 Complemen
7	91	100.0	41	8	ADT92344	Adt92344 Human com
8	91	100.0	63	5	AAB71451	Aab71451 Human C3
9	91	100.0	294	5	AAU74858	Aau74858 Complemen
10	91	100.0	294	5	AAU74866	Aau74866 Complemen
11	91	100.0	294	5	AAU74869	Aau74869 Complemen
12	91	100.0	294	5	AAU74855	Aau74855 Complemen
13	91	100.0	294	5	AAU74862	Aau74862 Complemen
14	91	100.0	294	5	AAU74859	Aau74859 Complemen
15	91	100.0	294	5	AAU74872	Aau74872 Complemen
16	91	100.0	294	5	AAU74873	Aau74873 Complemen
17	91	100.0	294	5	AAU74863	Aau74863 Complemen
18	91	100.0	294	5	AAU74856	Aau74856 Complemen
19	91	100.0	294	5	AAU74880	Aau74880 Complemen
20	91	100.0	294	5	AAU74860	Aau74860 Complemen
21	91	100.0	294	5	AAU74854	Aau74854 Complemen
22	91	100.0	294	5	AAU74865	Aau74865 Complemen
23	91	100.0	294	5	AAU74867	Aau74867 Complemen
24	91	100.0	294	5	AAU74861	Aau74861 Complemen
25	91	100.0	294	5	AAU74871	Aau74871 Complemen
26	91	100.0	294	5	AAU74868	Aau74868 Complemen
27	91	100.0	294	5	AAU74874	Aau74874 Complemen
28	91	100.0	294	5	AAU74878	Aau74878 Complemen
29	91	100.0	294	5	AAU74879	Aau74879 Complemen
30	91	100.0	294	5	AAU74857	Aau74857 Complemen
31	91	100.0	294	5	AAU74864	Aau74864 Complemen
32	91	100.0	294	5	AAU74870	Aau74870 Complemen
33	91	100.0	294	5	AAU74875	Aau74875 Complemen
34	91	100.0	294	5	AAU74876	Aau74876 Complemen
35	91	100.0	294	5	AAU74877	Aau74877 Complemen
36	91	100.0	294	5	AAU74881	Aau74881 Complemen
37	91	100.0	310	8	ADI05803	Adi05803 Human com
38	91	100.0	310	8	ADI05805	Adi05805 Human C3d
39	91	100.0	310	8	ADI05804	Adi05804 Human C3d
40	91	100.0	349	2	AAR10900	Aar10900 Human pho
41	91	100.0	349	2	AAR21776	Aar21776 Phospholi
42	91	100.0	349	2	AAR51949	Aar51949 Phospholi
43	91	100.0	370	8	ADK72548	Adk72548 Fusion pr
44	91	100.0	383	8	ADK72551	Adk72551 Fusion pr
45	91	100.0	387	8	ADK72549	Adk72549 Fusion pr

ALIGNMENTS

RESULT 1
AAB92360
ID AAB92360 standard; peptide; 16 AA.
XX
AC AAB92360;
XX
DT 22-JUN-2001 (first entry)
XX
DE Miscellaneous peptide SEQ ID NO:1536.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 707; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
||||||||||||||||
Db 1 KNRWEDPGKQLYNVEA 16

RESULT 2
ABP58217
ID ABP58217 standard; peptide; 16 AA.
XX
AC ABP58217;
XX
DT 21-MAR-2003 (first entry)
XX
DE Immunostimulant C3d peptide.
XX
KW Immunostimulant; C3d; human; fusion protein; tumour; vaccine; adjuvant.
XX
OS Homo sapiens.
XX
PN WO200297041-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016651.
XX
PR 29-MAY-2001; 2001US-00865281.
XX
PA (IMMP-) IMMPHERON INC.
PA (INNE-) INNEXUS CORP.
XX
PI Kohler H, Morgan C;
XX
DR WPI; 2003-140458/13.
XX
PT Novel fusion protein for use as molecular adjuvant, has an antibody and a
PT peptide with immunostimulatory, membrane transport or homophilic
PT activities, connected to the antibody by peptide bonds.
XX
PS Example 1; Page 14; 39pp; English.
XX
CC The present invention provides a fusion protein made up of an antibody
CC and a peptide having e.g. immunostimulant, membrane transport or
CC homophilic activity. The peptide is located at a site in the antibody
CC such that it does not compromise the antigen recognition of the antibody.
CC In order to enhance its activity, the peptide may be flanked by loop-
CC forming or conformation-conferring sequences. The present sequence is an
CC example of a suitable imunostimulatory peptide for use as a fusion
CC protein component. The peptide is derived from human C3d amino acids 1217
CC -1232. In examples from the invention, the C3d peptide was affinity cross
CC -linked to tumour anti-idiotype and tumour idiotype vaccine antibodies,
CC significantly enhancing the immune response to the tumour and protecting
CC against tumour challenge. The vaccination protocol did not include any
CC adjuvant, such as Freund's adjuvant or keyhole limpet haemocyanin
CC conjugation, both of which are not permissible by the FDA for human use
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
||||||||||||||||
Db 1 KNRWEDPGKQLYNVEA 16

RESULT 3
ADS17594
ID ADS17594 standard; peptide; 16 AA.
XX
AC ADS17594;
XX
DT 02-DEC-2004 (first entry)
XX
DE Peptide derived from the C3d peptide and affinity linked to 3H1 antibody.
XX
KW immunostimulatory; membrane transport; homophilic; signaling protein;
KW caspase; kinase; phosphatase; viral protein; tumour antigen;
KW nuclear protein; nucleolar protein; DNA synthesis; cytoskeletal protein;
KW cell proliferation; cytostasis; membrane transporter peptide;
KW Kaposi fibroblast factor; TAT peptide; HIV-1; antennapedia homeodomain;
KW herpes virus protein VP22; transportan peptide; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; C3d; 3H1; monoclonal antibody;
KW anti-idiotypic antibody; carcino-embryonic antigen; CEA;
KW anti-idiotype vaccine; antibody.
XX
OS Synthetic.
XX
PN WO2004078146-A2.
XX
PD 16-SEP-2004.
XX
PF 05-MAR-2004; 2004WO-US006911.
XX
PR 05-MAR-2003; 2003US-0451980P.
XX
PA (INNE-) INNEXUS BIOTECHNOLOGY INC.
PA (IMMP-) IMMPHERON INC.
XX
PI Kohler H, Muller S, Brown TL, Zhao Y, Morgan AC;
XX
DR WPI; 2004-653567/63.
XX
PT New compound for regulating normal or infected cell function comprising
PT an antibody conjugated to a membrane transporter peptide, useful in
PT preparing a composition for treating or preventing human diseases, e.g.
PT Alzheimer's disease.
XX
PS Example 1; SEQ ID NO 1; 50pp; English.
XX
CC The specification describes a fusion protein for regulating normal or
CC infected cell function, comprising an antibody conjugated to a peptide
CC having immunostimulatory, membrane transport, and homophilic activities.
CC The antibody is immunospecific for a signaling protein internal cell
CC consisting of caspases, kinases or phosphatases, an immature viral
CC protein, a cell-surface or intracellular tumour antigen, a nuclear or
CC nucleolar protein participating in regulation of DNA synthesis and gene
CC expression, or a cytoskeletal protein participating in cell proliferation
CC or cytostasis. The peptide portion of the fusion protein is preferably a
CC membrane transporter peptide that is endogenous to Kaposi fibroblast
CC factor, TAT peptides of HIV-1, antennapedia homeodomain-derived peptide,
CC herpes virus protein VP22, or transportan peptide. Fusion protein of the
CC invention are useful for preparing a composition for treating or
CC preventing human diseases, e.g., Alzheimer's disease, Huntington's
CC disease or Parkinson's disease. The present sequence represents a peptide
CC derived from the C3d region 1217-1232, which was affinity cross-linked
CC with 3H1 monoclonal antibody to produce fusion proteins of the invention.
CC 3H1 is a murine anti-idiotypic antibody which mimics the carcino-
CC embryonic antigen (CEA), and induces anti-CEA antibodies. The resulting
CC Cd3-3H1 fusion protein was used to enhance an anti-idiotype vaccine.
XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
||||||||||||||||
Db 1 KNRWEDPGKQLYNVEA 16

RESULT 4
ADV24825
ID ADV24825 standard; peptide; 16 AA.
XX
AC ADV24825;
XX
DT 24-FEB-2005 (first entry)
XX
DE CR2-binding complement C3d peptide, SEQ ID NO:2.
XX
KW Multivalent ligand; cell signaling; diagnostic; decontamination;
KW autoimmune disease; immune disorder; cancer; neoplasm; cancer metastasis;
KW immunosuppressive; immunomodulator; cytostatic; complement C3d.
XX
OS Unidentified.
XX
PN US2004248801-A1.
XX
PD 09-DEC-2004.
XX
PF 22-MAR-2004; 2004US-00806056.
XX
PR 21-MAR-2000; 2000US-0191014P.
PR 21-MAR-2001; 2001US-00815296.
PR 21-MAR-2003; 2003US-0456778P.
XX
PA (KIES/) KIESSLING L L.
PA (GRIF/) GRIFFITH B R.
PA (GEST/) GESTWICKI J E.
PA (STRO/) STRONG L.
XX
PI Kiessling LL, Griffith BR, Gestwicki JE, Strong L;
XX
DR WPI; 2005-046763/05.
XX
PT Novel multivalent ligand, useful for inducing biological response,
PT enhancing aggregation of biological particles and enhancing induction of
PT cellular response.
XX
PS Example 3; SEQ ID NO 2; 76pp; English.
XX
CC The invention relates to a multivalent ligand comprising a plurality of
CC signal recognition elements (SRE), binding recognition elements (BRE) and
CC functional elements (FE), and which is bonded to a polymeric scaffold.
CC The SREs are involved, either directly or indirectly, in biological
CC signaling processes, while the BREs facilitate the binding associated
CC with the process. Examples of SREs used in the multivalent ligand include
CC epitopes (especially one characteristic of a cancer cell), antigens,
CC antibodies or fragments thereof, cell surface receptors, polysaccharides,
CC nucleic acids or small drug-like compounds, and suitable BREs include
CC polysaccharides or metal-chelating groups which are optionally bound to
CC metals. The FE may be a detectable label, a reporter group or an enzyme.
CC The invention also relates to use of multivalent ligands in a method for
CC inducing a biological response in a biological system such as a cell or
CC organism which comprises one or more receptors recognized by an SRE; a
CC method of enhancing aggregation of biological particles such as cells or
CC viruses using a multivalent ligand complex which comprises several
CC recognition elements which each induce aggregation of one or more of the
CC biological particles; a method for inducing a cellular response or for
CC enhancing cellular response induction using a multivalent ligand; a
CC method of generating an assembly of biological macromolecules or
CC particles by providing a multivalent ligand comprising a molecular
CC scaffold to which several biological macromolecules or particles are
CC attached via BREs, wherein the number, density and spacing of the BREs is
CC controlled; and a library of multivalent ligands of the invention, in
CC which the members of the libraries vary in the type, number and/or
CC relative positioning of recognition elements, the combinations of BREs
CC and SREs present, the presence and/or positioning of spacers, the number
CC of repeating units or monomers, and the presence, type or number of FEs.
CC The invention also discloses pharmaceutical compositions comprising
CC multivalent ligands of the invention. The multivalent ligands are useful
CC for modulating immune system cell responses to epitopes, thereby
CC inhibiting or attenuating autoimmune disorders, and are also useful for
CC treating undesired cell proliferation (cancer) and undesired cell
CC migration (metastasis). They can be used in diagnostic applications for
CC the detection of biological molecules or particles in biological systems,
CC and are useful for preventing or inhibiting biofouling or removing
CC undesired cells in a selected environment. The present sequence
CC represents a complement C3d peptide able to bind complement receptor CR2
CC which may be used as a signal in a multivalent ligand for inducing an
CC enhanced immune response.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
||||||||||||||||
Db 1 KNRWEDPGKQLYNVEA 16

RESULT 5
ADV24829
ID ADV24829 standard; peptide; 17 AA.
XX
AC ADV24829;
XX
DT 24-FEB-2005 (first entry)
XX
DE Complement C3d derived peptide, SEQ ID NO:6.
XX
KW Multivalent ligand; cell signaling; diagnostic; decontamination;
KW autoimmune disease; immune disorder; cancer; neoplasm; cancer metastasis;
KW immunosuppressive; immunomodulator; cytostatic; complement C3d.
XX
OS Synthetic.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 17
FT /note= "The side chain thiol group is attached to the
FT polymer backbone of the multivalent ligand"
XX
PN US2004248801-A1.
XX
PD 09-DEC-2004.
XX
PF 22-MAR-2004; 2004US-00806056.
XX
PR 21-MAR-2000; 2000US-0191014P.
PR 21-MAR-2001; 2001US-00815296.
PR 21-MAR-2003; 2003US-0456778P.
XX
PA (KIES/) KIESSLING L L.
PA (GRIF/) GRIFFITH B R.
PA (GEST/) GESTWICKI J E.
PA (STRO/) STRONG L.
XX
PI Kiessling LL, Griffith BR, Gestwicki JE, Strong L;
XX
DR WPI; 2005-046763/05.
XX
PT Novel multivalent ligand, useful for inducing biological response,

PT enhancing aggregation of biological particles and enhancing induction of
PT cellular response.
XX
PS Example 3; SEQ ID NO 6; 76pp; English.
XX
CC The invention relates to a multivalent ligand comprising a plurality of
CC signal recognition elements (SRE), binding recognition elements (BRE) and
CC functional elements (FE), and which is bonded to a polymeric scaffold.
CC The SREs are involved, either directly or indirectly, in biological
CC signaling processes, while the BREs facilitate the binding associated
CC with the process. Examples of SREs used in the multivalent ligand include
CC epitopes (especially one characteristic of a cancer cell), antigens,
CC antibodies or fragments thereof, cell surface receptors, polysaccharides,
CC nucleic acids or small drug-like compounds, and suitable BREs include
CC polysaccharides or metal-chelating groups which are optionally bound to
CC metals. The FE may be a detectable label, a reporter group or an enzyme.
CC The invention also relates to use of multivalent ligands in a method for
CC inducing a biological response in a biological system such as a cell or
CC organism which comprises one or more receptors recognized by an SRE; a
CC method of enhancing aggregation of biological particles such as cells or
CC viruses using a multivalent ligand complex which comprises several
CC recognition elements which each induce aggregation of one or more of the
CC biological particles; a method for inducing a cellular response or for
CC enhancing cellular response induction using a multivalent ligand; a
CC method of generating an assembly of biological macromolecules or
CC particles by providing a multivalent ligand comprising a molecular
CC scaffold to which several biological macromolecules or particles are
CC attached via BREs, wherein the number, density and spacing of the BREs is
CC controlled; and a library of multivalent ligands of the invention, in
CC which the members of the libraries vary in the type, number and/or
CC relative positioning of recognition elements, the combinations of BREs
CC and SREs present, the presence and/or positioning of spacers, the number
CC of repeating units or monomers, and the presence, type or number of FEs.
CC The invention also discloses pharmaceutical compositions comprising
CC multivalent ligands of the invention. The multivalent ligands are useful
CC for modulating immune system cell responses to epitopes, thereby
CC inhibiting or attenuating autoimmune disorders, and are also useful for
CC treating undesired cell proliferation (cancer) and undesired cell
CC migration (metastasis). They can be used in diagnostic applications for
CC the detection of biological molecules or particles in biological systems,
CC and are useful for preventing or inhibiting biofouling or removing
CC undesired cells in a selected environment. Sequences ADV24828-ADV24829
CC represent peptides derived from the complement C3d peptide of ADV24825
CC which are attached via a thiol group to a multivalent ligand for the
CC induction of an enhanced immune response.
XX
SQ Sequence 17 AA;

```
  Query Match             100.0%;  Score 91;  DB 9;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16
```

RESULT 6
ADV24828
ID ADV24828 standard; peptide; 17 AA.
XX
AC ADV24828;
XX
DT 24-FEB-2005 (first entry)
XX
DE Complement C3d derived peptide, SEQ ID NO:5.
XX
KW Multivalent ligand; cell signaling; diagnostic; decontamination;
KW autoimmune disease; immune disorder; cancer; neoplasm; cancer metastasis;
KW immunosuppressive; immunomodulator; cytostatic; complement C3d.
XX
OS Synthetic.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "The side chain thiol group is attached to the
FT polymer backbone of the multivalent ligand"
XX
PN US2004248801-A1.
XX
PD 09-DEC-2004.
XX
PF 22-MAR-2004; 2004US-00806056.
XX
PR 21-MAR-2000; 2000US-0191014P.
PR 21-MAR-2001; 2001US-00815296.
PR 21-MAR-2003; 2003US-0456778P.
XX
PA (KIES/) KIESSLING L L.
PA (GRIF/) GRIFFITH B R.
PA (GEST/) GESTWICKI J E.
PA (STRO/) STRONG L.
XX
PI Kiessling LL, Griffith BR, Gestwicki JE, Strong L;
XX
DR WPI; 2005-046763/05.
XX
PT Novel multivalent ligand, useful for inducing biological response,
PT enhancing aggregation of biological particles and enhancing induction of
PT cellular response.
XX
PS Example 3; SEQ ID NO 5; 76pp; English.
XX
CC The invention relates to a multivalent ligand comprising a plurality of
CC signal recognition elements (SRE), binding recognition elements (BRE) and
CC functional elements (FE), and which is bonded to a polymeric scaffold.
CC The SREs are involved, either directly or indirectly, in biological
CC signaling processes, while the BREs facilitate the binding associated
CC with the process. Examples of SREs used in the multivalent ligand include
CC epitopes (especially one characteristic of a cancer cell), antigens,
CC antibodies or fragments thereof, cell surface receptors, polysaccharides,
CC nucleic acids or small drug-like compounds, and suitable BREs include
CC polysaccharides or metal-chelating groups which are optionally bound to
CC metals. The FE may be a detectable label, a reporter group or an enzyme.
CC The invention also relates to use of multivalent ligands in a method for
CC inducing a biological response in a biological system such as a cell or
CC organism which comprises one or more receptors recognized by an SRE; a
CC method of enhancing aggregation of biological particles such as cells or
CC viruses using a multivalent ligand complex which comprises several
CC recognition elements which each induce aggregation of one or more of the
CC biological particles; a method for inducing a cellular response or for
CC enhancing cellular response induction using a multivalent ligand; a
CC method of generating an assembly of biological macromolecules or
CC particles by providing a multivalent ligand comprising a molecular
CC scaffold to which several biological macromolecules or particles are
CC attached via BREs, wherein the number, density and spacing of the BREs is
CC controlled; and a library of multivalent ligands of the invention, in
CC which the members of the libraries vary in the type, number and/or
CC relative positioning of recognition elements, the combinations of BREs
CC and SREs present, the presence and/or positioning of spacers, the number
CC of repeating units or monomers, and the presence, type or number of FEs.
CC The invention also discloses pharmaceutical compositions comprising
CC multivalent ligands of the invention. The multivalent ligands are useful
CC for modulating immune system cell responses to epitopes, thereby
CC inhibiting or attenuating autoimmune disorders, and are also useful for
CC treating undesired cell proliferation (cancer) and undesired cell
CC migration (metastasis). They can be used in diagnostic applications for
CC the detection of biological molecules or particles in biological systems,
CC and are useful for preventing or inhibiting biofouling or removing
CC undesired cells in a selected environment. Sequences ADV24828-ADV24829
CC represent peptides derived from the complement C3d peptide of ADV24825
CC which are attached via a thiol group to a multivalent ligand for the
CC induction of an enhanced immune response.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 91; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
Db 2 KNRWEDPGKQLYNVEA 17

RESULT 7
ADT92344
ID ADT92344 standard; peptide; 41 AA.
XX
AC ADT92344;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human complement C3 peptide, a marker for colorectal cancer Seq 40.
XX
KW colorectal cancer; quantitative detection assay; protein chip technology;
KW mass spectrometry; cell proliferation; complement C3.
XX
OS Homo sapiens.
XX
PN WO2004090550-A2.
XX
PD 21-OCT-2004.
XX
PF 07-APR-2004; 2004WO-DK000263.
XX
PR 08-APR-2003; 2003DK-00000541.
PR 16-JUL-2003; 2003DK-00001085.
XX
PA (COLO-) COLOTECH AS.
PA (RASK/) RASKOV H H.
XX
PI Raskov HH, Albrethsen J, Gammeltoft S, Bogebo RM;
XX
DR WPI; 2004-766501/75.
XX
PT Diagnosing colorectal cancer in sample from mammal, involves use of
PT marker polypeptides having specific molecular weights and degradation
PT product of human serum albumin.
XX
PS Example 19; SEQ ID NO 40; 132pp; English.
XX
CC This invention relates to a novel method for diagnosing human colorectal
CC cancer using novel protein markers. Specifically, it refers to a
CC quantitative detection assay that uses at least one marker chosen from
CC polypeptides having apparent molecular weights ranging between 1005Da and
CC 66800Da, and compares the signal intensity of the marker against a
CC reference value from a healthy person. As such, the present invention
CC describes a method that can be used to diagnose persons with colorectal
CC cancer by means of protein chip technology using mass spectrometry, by
CC identifying differential expression of markers that are indicative of
CC cell proliferation. Preferred protein markers include alpha-fibrinogen
CC protein and human serum albumin where a preferred kit enables detection
CC of a combination of two or more proteins. Accordingly, this method is
CC useful for diagnosing colorectal cancer, as well as predicting clinical
CC outcomes, complications and mortality of an individual already diagnosed
CC with the disease. This peptide sequence is a human complement C3 peptide,
CC an down-regulated blood protein marker for colorectal cancer given in an
CC exemplification of the invention.
XX
SQ Sequence 41 AA;

Query Match 100.0%; Score 91; DB 8; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
Db 14 KNRWEDPGKQLYNVEA 29

RESULT 8
AAB71451
ID AAB71451 standard; peptide; 63 AA.
XX
AC AAB71451;
XX
DT 11-DEC-2002 (first entry)
XX
DE Human C3 discontinous Factor H binding site SEQ ID 20.
XX
KW CVF1; cobra venom factor; proCVF1; cobra; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; vasotropic; vulnerary; septic shock;
KW antiinflammatory; antibacterial; decomplementation; rheumatoid arthritis;
KW ischaemia-reperfusion injury; thermal injury; lupus erythematosus;
KW respiratory distress syndrome; tissue rejection; complement; tumour;
KW xenotransplantation; gene therapy; burn; cancer.
XX
OS Homo sapiens.
XX
PN US2002103346-A1.
XX
PD 01-AUG-2002.
XX
PF 10-AUG-2001; 2001US-00925442.
XX
PR 14-JUN-1996; 96US-00662227.
PR 03-FEB-1998; 98US-00017947.
XX
PA (GEOU) UNIV GEORGETOWN.
XX
PI Vogel C, Bredehorst R, Fritzinger D, Kock M;
XX
DR WPI; 2002-690629/74.
XX
PT Novel recombinant pro-cobra venom factor polypeptide useful for
PT decomplementation of animal suffering from septic shock, ischemia-
PT reperfusion injury, arthritis, respiratory distress syndrome, or tissue
PT rejection.
XX
PS Example; Fig 7B; 82pp; English.
XX
CC This invention describes a novel recombinant pro-cobra venom factor
CC polypeptide which has antirheumatic, antiarthritic, dermatological,
CC immunosuppressive, vasotropic, vulnerary, antiinflammatory, antibacterial
CC and cytostatic activity. The polypeptide of the invention is useful for
CC decomplementation by administering proCVF to an animal such as reptile,
CC fish, bird or mammal such as guinea pigs, mice, rats, pigs, baboons,
CC chimps, dogs, cats, horses, cows or humans, suffering from septic shock,
CC ischaemia-reperfusion injury, thermal injury, arthritis, lupus,
CC respiratory distress syndrome, or a tissue rejection. ProCVF is useful as
CC research agent to deplete the complement activity in the plasma of
CC laboratory animals in vitro and in vivo, as therapeutic agent in humans
CC for treating cancer, for antibody targeting to tumour cells, for
CC depleting complement in patients undergoing xenotransplantation to
CC suppress the hyperacute rejection of the foreign organ, for temporary
CC depletion of complement in patient undergoing gene therapy using
CC retroviral vectors, and for treating diseases with circulating immune
CC complexes e.g. rheumatoid arthritis, lupus erythematosus, septic shock,
CC adult respiratory distress syndrome, ischaemic-reperfusion injury and
CC thermal injury from burns. This sequence represents a fragment of protein
CC described in the disclosure of the invention
XX
SQ Sequence 63 AA;

Query Match 100.0%; Score 91; DB 5; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16

```
Db          9 KNRWEDPGKQLYNVEA 24


RESULT 9
AAU74858
ID   AAU74858 standard; protein; 294 AA.
XX
AC   AAU74858;
XX
DT   09-APR-2002  (first entry)
XX
DE   Complement pathway protein C3d, R49A mutant.
XX
KW   Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
KW   vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 49
FT                   /note= "Wild type Arg substituted by Ala"
XX
PN   WO200192295-A2.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-CA000785.
XX
PR   30-MAY-2000; 2000US-0207434P.
XX
PA   (UTOR ) UNIV TORONTO.
XX
PI   Isenman DE,  Clemenza L;
XX
DR   WPI; 2002-114323/15.
XX
PT   Ligand useful for modulating immune response such as in the preparation
PT   of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
PS   Disclosure; Page; 53pp; English.
XX
CC   The invention describes a ligand of the complement receptor 2 (CD21 or
CC   CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
CC   molecule. The ligand is useful in the manufacture of a medicament such as
CC   a vaccine for modulating the immune response of a host (preferably tumour
CC   vaccine), and as antigens in immunogenic compositions, therapeutics
CC   diagnostic reagents, in the generation of diagnostic agents and as cancer
CC   therapeutics. The ligand has the ability to bind CD21 and stimulate B
CC   cells through the CD21/CD19 complex. Non-naturally occurring ligands and
CC   site specific mutated analogues of C3d demonstrate an enhanced binding
CC   affinity for CD21 as compared to the binding affinity of a wild-type C3d
CC   molecule. The ligand alters the immunogenicity of an antigen, e.g. by
CC   inducing or enhancing an immune response to an antigen in a host and thus
CC   protects the host against disease caused by the pathogen. This sequence
CC   represents the complement pathway protein C3d R49A mutant, used to study
CC   the interaction of C3d with complement receptor 2 (CD21/CD2), described
CC   in the method of the invention. Note: This sequence does not appear in
CC   the specification but has been created from a C3d wild type sequence
CC   referenced on page 11 of the invention
XX
SQ   Sequence 294 AA;

  Query Match             100.0%;  Score 91;  DB 5;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 10
AAU74866
ID   AAU74866 standard; protein; 294 AA.
XX
AC   AAU74866;
XX
DT   09-APR-2002  (first entry)
XX
DE   Complement pathway protein C3d, N98A mutant.
XX
KW   Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
KW   vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 98
FT                   /note= "Wild type Asn substituted by Ala"
XX
PN   WO200192295-A2.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-CA000785.
XX
PR   30-MAY-2000; 2000US-0207434P.
XX
PA   (UTOR ) UNIV TORONTO.
XX
PI   Isenman DE,  Clemenza L;
XX
DR   WPI; 2002-114323/15.
XX
PT   Ligand useful for modulating immune response such as in the preparation
PT   of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
PS   Disclosure; Page; 53pp; English.
XX
CC   The invention describes a ligand of the complement receptor 2 (CD21 or
CC   CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
CC   molecule. The ligand is useful in the manufacture of a medicament such as
CC   a vaccine for modulating the immune response of a host (preferably tumour
CC   vaccine), and as antigens in immunogenic compositions, therapeutics
CC   diagnostic reagents, in the generation of diagnostic agents and as cancer
CC   therapeutics. The ligand has the ability to bind CD21 and stimulate B
CC   cells through the CD21/CD19 complex. Non-naturally occurring ligands and
CC   site specific mutated analogues of C3d demonstrate an enhanced binding
CC   affinity for CD21 as compared to the binding affinity of a wild-type C3d
CC   molecule. The ligand alters the immunogenicity of an antigen, e.g. by
CC   inducing or enhancing an immune response to an antigen in a host and thus
CC   protects the host against disease caused by the pathogen. This sequence
CC   represents the complement pathway protein C3d N98A mutant, used to study
CC   the interaction of C3d with complement receptor 2 (CD21/CD2), described
CC   in the method of the invention. Note: This sequence does not appear in
CC   the specification but has been created from a C3d wild type sequence
CC   referenced on page 11 of the invention
XX
SQ   Sequence 294 AA;

  Query Match             100.0%;  Score 91;  DB 5;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 11
AAU74869
ID   AAU74869 standard; protein; 294 AA.
XX
AC   AAU74869;
```

```
XX
DT   09-APR-2002  (first entry)
XX
DE   Complement pathway protein C3d, D163A mutant.
XX
KW   Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
KW   vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 163
FT                   /note= "Wild type Asp substituted by Ala"
XX
PN   WO200192295-A2.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-CA000785.
XX
PR   30-MAY-2000; 2000US-0207434P.
XX
PA   (UTOR ) UNIV TORONTO.
XX
PI   Isenman DE,  Clemenza L;
XX
DR   WPI; 2002-114323/15.
XX
PT   Ligand useful for modulating immune response such as in the preparation
PT   of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
PS   Disclosure; Page; 53pp; English.
XX
CC   The invention describes a ligand of the complement receptor 2 (CD21 or
CC   CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
CC   molecule. The ligand is useful in the manufacture of a medicament such as
CC   a vaccine for modulating the immune response of a host (preferably tumour
CC   vaccine), and as antigens in immunogenic compositions, therapeutics
CC   diagnostic reagents, in the generation of diagnostic agents and as cancer
CC   therapeutics. The ligand has the ability to bind CD21 and stimulate B
CC   cells through the CD21/CD19 complex. Non-naturally occurring ligands and
CC   site specific mutated analogues of C3d demonstrate an enhanced binding
CC   affinity for CD21 as compared to the binding affinity of a wild-type C3d
CC   molecule. The ligand alters the immunogenicity of an antigen, e.g. by
CC   inducing or enhancing an immune response to an antigen in a host and thus
CC   protects the host against disease caused by the pathogen. This sequence
CC   represents the complement pathway protein C3d D163A mutant, used to study
CC   the interaction of C3d with complement receptor 2 (CD21/CD2), described
CC   in the method of the invention. Note: This sequence does not appear in
CC   the specification but has been created from a C3d wild type sequence
CC   referenced on page 11 of the invention
XX
SQ   Sequence 294 AA;

  Query Match             100.0%;  Score 91;  DB 5;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 12
AAU74855
ID   AAU74855 standard; protein; 294 AA.
XX
AC   AAU74855;
XX
DT   09-APR-2002  (first entry)
XX
DE   Complement pathway protein C3d, E37A mutant.
XX
KW   Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
KW   vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 37
FT                   /note= "Wild type Glu substituted by Ala"
XX
PN   WO200192295-A2.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-CA000785.
XX
PR   30-MAY-2000; 2000US-0207434P.
XX
PA   (UTOR ) UNIV TORONTO.
XX
PI   Isenman DE,  Clemenza L;
XX
DR   WPI; 2002-114323/15.
XX
PT   Ligand useful for modulating immune response such as in the preparation
PT   of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
PS   Disclosure; Page; 53pp; English.
XX
CC   The invention describes a ligand of the complement receptor 2 (CD21 or
CC   CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
CC   molecule. The ligand is useful in the manufacture of a medicament such as
CC   a vaccine for modulating the immune response of a host (preferably tumour
CC   vaccine), and as antigens in immunogenic compositions, therapeutics
CC   diagnostic reagents, in the generation of diagnostic agents and as cancer
CC   therapeutics. The ligand has the ability to bind CD21 and stimulate B
CC   cells through the CD21/CD19 complex. Non-naturally occurring ligands and
CC   site specific mutated analogues of C3d demonstrate an enhanced binding
CC   affinity for CD21 as compared to the binding affinity of a wild-type C3d
CC   molecule. The ligand alters the immunogenicity of an antigen, e.g. by
CC   inducing or enhancing an immune response to an antigen in a host and thus
CC   protects the host against disease caused by the pathogen. This sequence
CC   represents the complement pathway protein C3d E37A mutant, used to study
CC   the interaction of C3d with complement receptor 2 (CD21/CD2), described
CC   in the method of the invention. Note: This sequence does not appear in
CC   the specification but has been created from a C3d wild type sequence
CC   referenced on page 11 of the invention
XX
SQ   Sequence 294 AA;

  Query Match             100.0%;  Score 91;  DB 5;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 13
AAU74862
ID   AAU74862 standard; protein; 294 AA.
XX
AC   AAU74862;
XX
DT   09-APR-2002  (first entry)
XX
DE   Complement pathway protein C3d, E37A/E39A mutant.
XX
KW   Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
KW   vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX
```

```
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 37
FT                   /note= "Wild type Glu substituted by Ala"
FT   Misc-difference 39
FT                   /note= "Wild type Glu substituted by Ala"
XX
PN   WO200192295-A2.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-CA000785.
XX
PR   30-MAY-2000; 2000US-0207434P.
XX
PA   (UTOR ) UNIV TORONTO.
XX
PI   Isenman DE,  Clemenza L;
XX
DR   WPI; 2002-114323/15.
XX
PT   Ligand useful for modulating immune response such as in the preparation
PT   of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
PS   Disclosure; Page; 53pp; English.
XX
CC   The invention describes a ligand of the complement receptor 2 (CD21 or
CC   CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
CC   molecule. The ligand is useful in the manufacture of a medicament such as
CC   a vaccine for modulating the immune response of a host (preferably tumour
CC   vaccine), and as antigens in immunogenic compositions, therapeutics
CC   diagnostic reagents, in the generation of diagnostic agents and as cancer
CC   therapeutics. The ligand has the ability to bind CD21 and stimulate B
CC   cells through the CD21/CD19 complex. Non-naturally occurring ligands and
CC   site specific mutated analogues of C3d demonstrate an enhanced binding
CC   affinity for CD21 as compared to the binding affinity of a wild-type C3d
CC   molecule. The ligand alters the immunogenicity of an antigen, e.g. by
CC   inducing or enhancing an immune response to an antigen in a host and thus
CC   protects the host against disease caused by the pathogen. This sequence
CC   represents the complement pathway protein C3d E37A/E39A mutant, used to
CC   study the interaction of C3d with complement receptor 2 (CD21/CD2),
CC   described in the method of the invention. Note: This sequence does not
CC   appear in the specification but has been created from a C3d wild type
CC   sequence referenced on page 11 of the invention
XX
SQ   Sequence 294 AA;

  Query Match             100.0%;  Score 91;  DB 5;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 14
AAU74859
ID   AAU74859 standard; protein; 294 AA.
XX
AC   AAU74859;
XX
DT   09-APR-2002  (first entry)
XX
DE   Complement pathway protein C3d, R49M mutant.
XX
KW   Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
KW   vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 49
FT                   /note= "Wild type Arg substituted by Met"
XX
PN   WO200192295-A2.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-CA000785.
XX
PR   30-MAY-2000; 2000US-0207434P.
XX
PA   (UTOR ) UNIV TORONTO.
XX
PI   Isenman DE,  Clemenza L;
XX
DR   WPI; 2002-114323/15.
XX
PT   Ligand useful for modulating immune response such as in the preparation
PT   of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
PS   Disclosure; Page; 53pp; English.
XX
CC   The invention describes a ligand of the complement receptor 2 (CD21 or
CC   CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
CC   molecule. The ligand is useful in the manufacture of a medicament such as
CC   a vaccine for modulating the immune response of a host (preferably tumour
CC   vaccine), and as antigens in immunogenic compositions, therapeutics
CC   diagnostic reagents, in the generation of diagnostic agents and as cancer
CC   therapeutics. The ligand has the ability to bind CD21 and stimulate B
CC   cells through the CD21/CD19 complex. Non-naturally occurring ligands and
CC   site specific mutated analogues of C3d demonstrate an enhanced binding
CC   affinity for CD21 as compared to the binding affinity of a wild-type C3d
CC   molecule. The ligand alters the immunogenicity of an antigen, e.g. by
CC   inducing or enhancing an immune response to an antigen in a host and thus
CC   protects the host against disease caused by the pathogen. This sequence
CC   represents the complement pathway protein C3d R49M mutant, used to study
CC   the interaction of C3d with complement receptor 2 (CD21/CD2), described
CC   in the method of the invention. Note: This sequence does not appear in
CC   the specification but has been created from a C3d wild type sequence
CC   referenced on page 11 of the invention
XX
SQ   Sequence 294 AA;

  Query Match             100.0%;  Score 91;  DB 5;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db        224 KNRWEDPGKQLYNVEA 239


RESULT 15
AAU74872
ID   AAU74872 standard; protein; 294 AA.
XX
AC   AAU74872;
XX
DT   09-APR-2002  (first entry)
XX
DE   Complement pathway protein C3d, E166A mutant.
XX
KW   Complement; receptor; CD21; CD2; C3d; immune response; B cell stimulator;
KW   vaccine; CD21/CD19 complex; tumour; cancer; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 166
FT                   /note= "Wild type Glu substituted by Ala"
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XX
PN WO200192295-A2.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-CA000785.
XX
PR 30-MAY-2000; 2000US-0207434P.
XX
PA (UTOR) UNIV TORONTO.
XX
PI Isenman DE, Clemenza L;
XX
DR WPI; 2002-114323/15.
XX
PT Ligand useful for modulating immune response such as in the preparation
PT of vaccine comprises CD21 contacting amino acid residues of C3d molecule.
XX
PS Disclosure; Page; 53pp; English.
XX
CC The invention describes a ligand of the complement receptor 2 (CD21 or
CC CD2) comprising amino acid residues 36-39 and 160-167 of the C3d
CC molecule. The ligand is useful in the manufacture of a medicament such as
CC a vaccine for modulating the immune response of a host (preferably tumour
CC vaccine), and as antigens in immunogenic compositions, therapeutics
CC diagnostic reagents, in the generation of diagnostic agents and as cancer
CC therapeutics. The ligand has the ability to bind CD21 and stimulate B
CC cells through the CD21/CD19 complex. Non-naturally occurring ligands and
CC site specific mutated analogues of C3d demonstrate an enhanced binding
CC affinity for CD21 as compared to the binding affinity of a wild-type C3d
CC molecule. The ligand alters the immunogenicity of an antigen, e.g. by
CC inducing or enhancing an immune response to an antigen in a host and thus
CC protects the host against disease caused by the pathogen. This sequence
CC represents the complement pathway protein C3d E166A mutant, used to study
CC the interaction of C3d with complement receptor 2 (CD21/CD2), described
CC in the method of the invention. Note: This sequence does not appear in
CC the specification but has been created from a C3d wild type sequence
CC referenced on page 11 of the invention
XX
SQ Sequence 294 AA;

Query Match 100.0%; Score 91; DB 5; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
||||||||||||||||
Db 224 KNRWEDPGKQLYNVEA 239

Search completed: May 15, 2006, 16:12:19
Job time : 186 secs

GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 15, 2006, 16:09:21 ; Search time 229 Seconds
(without alignments)
49.295 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	100.0	1663	1	CO3_HUMAN	P01024 h complemen
2	80	87.9	1663	1	CO3_RAT	P01026 rattus norv
3	79	86.8	726	1	CO3_RABIT	P12247 oryctolagus
4	77	84.6	349	2	O46544_SHEEP	O46544 ovis aries
5	76	83.5	154	2	Q29289_PIG	Q29289 sus scrofa
6	76	83.5	310	2	Q9Z115_MESAU	Q9z115 mesocricetu
7	73	80.2	303	2	Q693V9_BOVIN	Q693v9 bos taurus
8	73	80.2	1663	1	CO3_MOUSE	P01027 m complemen
9	73	80.2	1663	2	Q80XP1_MOUSE	Q80xp1 mus musculu
10	71	78.0	1661	2	Q9GKP1_PIG	Q9gkp1 sus scrofa
11	58	63.7	1666	1	CO3_CAVPO	P12387 cavia porce
12	52	57.1	1399	1	R1_ARATH	Q9sac6 arabidopsis
13	52	57.1	1540	2	Q9SGX4_ARATH	Q9sgx4 arabidopsis
14	51	56.0	1188	2	Q57UI3_9TRYP	Q57ui3 trypanosoma
15	50	54.9	92	2	Q9MXA7_BARIN	Q9mxa7 barbus inte
16	48	52.7	922	2	Q8XIG1_CLOPE	Q8xig1 clostridium
17	47.5	52.2	373	2	Q9F2H7_STAHA	Q9f2h7 staphylococ
18	47.5	52.2	401	2	Q8DYL9_STRA5	Q8dyl9 streptococc
19	47.5	52.2	401	2	Q8E475_STRA3	Q8e475 streptococc
20	47	51.6	782	2	Q4WMN5_ASPFU	Q4wmn5 aspergillus
21	46.5	51.1	462	1	TILS_ENTFA	Q839b3 enterococcu
22	46	50.5	79	2	Q5K4Z2_BARIN	Q5k4z2 barbus inte
23	46	50.5	79	2	Q5K4Z3_BARIN	Q5k4z3 barbus inte
24	46	50.5	79	2	Q5K505_BARIN	Q5k505 barbus inte
25	46	50.5	79	2	Q5K511_BARIN	Q5k511 barbus inte
26	46	50.5	79	2	Q5K516_BARIN	Q5k516 barbus inte
27	46	50.5	79	2	Q5K520_BARIN	Q5k520 barbus inte
28	46	50.5	79	2	Q5K522_BARIN	Q5k522 barbus inte
29	46	50.5	79	2	Q5K535_BARIN	Q5k535 barbus inte
30	46	50.5	79	2	Q5K540_BARIN	Q5k540 barbus inte
31	46	50.5	92	2	Q9MXB8_BARIN	Q9mxb8 barbus inte
32	46	50.5	151	2	P91717_DUGTI	P91717 dugesia tig
33	46	50.5	192	2	Q58RX6_9HIV1	Q58rx6 human immun
34	46	50.5	283	2	Q4RX02_TETNG	Q4rx02 tetraodon n
35	46	50.5	329	2	Q70XU5_BARIN	Q70xu5 barbus inte
36	46	50.5	400	2	Q92270_RHIOL	Q92270 rhizopus ol
37	46	50.5	467	2	Q8VUW4_STAHO	Q8vuw4 staphylococ
38	46	50.5	546	2	Q6AP19_DESPS	Q6ap19 desulfotale
39	46	50.5	652	2	Q5CLU8_CRYHO	Q5clu8 cryptospori
40	46	50.5	788	2	Q4IKE0_GIBZE	Q4ike0 gibberella
41	46	50.5	1475	1	R1_CITRE	Q8lpt9 citrus reti
42	45	49.5	172	2	Q7ZTW3_BRARE	Q7ztw3 brachydanio
43	45	49.5	260	2	Q6NY31_BRARE	Q6ny31 brachydanio
44	45	49.5	670	2	Q5GX45_XANOR	Q5gx45 xanthomonas
45	45	49.5	1684	2	Q9DDV9_ONCMY	Q9ddv9 oncorhynchu

ALIGNMENTS

RESULT 1
CO3_HUMAN
ID CO3_HUMAN STANDARD; PRT; 1663 AA.
AC P01024;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Complement C3 precursor [Contains: Complement C3 beta chain;
DE Complement C3 alpha chain; C3a anaphylatoxin; Complement C3b alpha'
DE chain; Complement C3c fragment; Complement C3dg fragment; Complement
DE C3g fragment; Complement C3d fragment; C3f fragment].
GN Name=C3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85140166; PubMed=2579379;
RA de Bruijn M.H.L., Fey G.H.;
RT "Human complement component C3: cDNA coding sequence and derived
RT primary structure.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:708-712(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLY-102; PRO-314;
RP LYS-863; ASP-1224 AND THR-1367.
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP PROTEIN SEQUENCE OF 672-748.
RX MEDLINE=76069169; PubMed=1238393;
RA Hugli T.E.;
RT "Human anaphylatoxin (C3a) from the third component of complement.
RT Primary structure.";
RL J. Biol. Chem. 250:8293-8301(1975).
RN [4]
RP PROTEIN SEQUENCE OF 955-966, AND SUBUNITS.
RC TISSUE=Serum;
RX MEDLINE=95293954; PubMed=7539791; DOI=10.1074/jbc.270.23.13645;
RA Oxvig C., Häaning J., Kristensen L., Wagner J.M., Rubin I.,
RA Stigbrand T., Gleich G.J., Sottrup-Jensen L.;
RT "Identification of angiotensinogen and complement C3dg as novel
RT proteins binding the proform of eosinophil major basic protein in
RT human pregnancy serum and plasma.";
RL J. Biol. Chem. 270:13645-13651(1995).
RN [5]
RP PROTEIN SEQUENCE OF 988-1036.
RX MEDLINE=82174534; PubMed=6175959;
RA Thomas M.L., Janatova J., Gray W.R., Tack B.F.;
RT "Third component of human complement: localization of the internal

```
RT   thiolester bond.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:1054-1058(1982).
RN   [6]
RP   PROTEIN SEQUENCE OF 1409-1563.
RX   MEDLINE=88154452; PubMed=3279119;
RA   Daoudaki M.E., Becherer J.D., Lambris J.D.;
RT   "A 34-amino acid peptide of the third component of complement mediates
RT   properdin binding.";
RL   J. Immunol. 140:1577-1580(1988).
RN   [7]
RP   STRUCTURE BY NMR OF C3A.
RX   MEDLINE=88276894; PubMed=3260670;
RA   Nettesheim D.G., Edalji R.P., Mollison K.W., Greer J.,
RA   Zuiderweg E.R.P.;
RT   "Secondary structure of complement component C3a anaphylatoxin in
RT   solution as determined by NMR spectroscopy: differences between
RT   crystal and solution conformations.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:5036-5040(1988).
RN   [8]
RP   MUTAGENESIS OF THIOESTER BOND REGION.
RX   MEDLINE=92250565; PubMed=1577777;
RA   Isaac L., Isenman D.E.;
RT   "Structural requirements for thioester bond formation in human
RT   complement component C3. Reassessment of the role of thioester bond
RT   integrity on the conformation of C3.";
RL   J. Biol. Chem. 267:10062-10069(1992).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE=93106233; PubMed=8416818; DOI=10.1016/0014-5793(93)81139-Q;
RA   Dolmer K., Sottrup-Jensen L.;
RT   "Disulfide bridges in human complement component C3b.";
RL   FEBS Lett. 315:85-90(1993).
RN   [10]
RP   CARBOHYDRATE-LINKAGE SITE ASN-85.
RX   MEDLINE=22660472; PubMed=12754519; DOI=10.1038/nbt827;
RA   Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT   "Identification and quantification of N-linked glycoproteins using
RT   hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL   Nat. Biotechnol. 21:660-666(2003).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 996-1303.
RX   MEDLINE=98259089; PubMed=9596584; DOI=10.1126/science.280.5367.1277;
RA   Nagar B., Jones R.G., Diefenbach R.J., Isenman D.E., Rini J.M.;
RT   "X-ray crystal structure of C3d: a C3 fragment and ligand for
RT   complement receptor 2.";
RL   Science 280:1277-1281(1998).
RN   [12]
RP   VARIANT C3S ASN-1216.
RX   MEDLINE=89309808; PubMed=2473125;
RA   Poznansky M.C., Clissold P.M., Lachmann P.J.;
RT   "The difference between human C3F and C3S results from a single amino
RT   acid change from an asparagine to an aspartate residue at position
RT   1216 on the alpha-chain of the complement component, C3.";
RL   J. Immunol. 143:1254-1258(1989).
RN   [13]
RP   ERRATUM, AND RETRACTION.
RX   MEDLINE=90063087; PubMed=2584723;
RA   Poznansky M.C., Clissold P.M., Lachmann P.J.;
RL   J. Immunol. 143:3860-3862(1989).
RN   [14]
RP   VARIANTS GLY-102 AND PRO-314.
RX   MEDLINE=91011240; PubMed=1976733; DOI=10.1084/jem.172.4.1011;
RA   Botto M., Yong Fong K., So A.K., Koch C., Walport M.J.;
RT   "Molecular basis of polymorphisms of human complement component C3.";
RL   J. Exp. Med. 172:1011-1017(1990).
RN   [15]
RP   VARIANT C3 DEFICIENCY ASN-549.
RX   MEDLINE=95050640; PubMed=7961791;
RA   Singer L., Whitehead W.T., Akama H., Katz Y., Fishelson Z.,
RA   Wetsel R.A.;
RT   "Inherited human complement C3 deficiency. An amino acid substitution
RT   in the beta-chain (Asp549 to Asn) impairs C3 secretion.";
RL   J. Biol. Chem. 269:28494-28499(1994).
RN   [16]
RP   VARIANT C3 DEFICIENCY GLN-1320.
RA   Watanabe Y., Matsui N., Yan K., Nishimukai H., Tokunaga K., Juji T.,
RA   Kobayashi N., Kohsaka T.;
RT   "A novel C3 allotype C3'F02'has an amino acid substitution that may
RT   inhibit iC3b synthesis and cause C3-hypocomplementemia.";
RL   Mol. Immunol. 30:62-62(1993).
CC   -!- FUNCTION: C3 plays a central role in the activation of the
CC       complement system. Its processing by C3 convertase is the central
CC       reaction in both classical and alternative complement pathways.
CC       After activation C3b can bind covalently, via its reactive
CC       thiolester, to cell surface carbohydrates or immune aggregates.
CC   -!- FUNCTION: Derived from proteolytic degradation of complement C3,
CC       C3a anaphylatoxin is a mediator of local inflammatory process. It
CC       induces the contraction of smooth muscle, increases vascular
CC       permeability and causes histamine release from mast cells and
CC       basophilic leukocytes.
CC   -!- SUBUNIT: C3 precursor is first processed by the removal of 4 Arg
CC       residues, forming two chains, beta and alpha, linked by a
CC       disulfide bond. C3 convertase activates C3 by cleaving the alpha
CC       chain, releasing C3a anaphylatoxin and generating C3b (beta chain
CC       + alpha' chain). During pregnancy, C3dg exists as a complex
CC       (probably a 2:2:2 heterohexamer) with AGT and the proform of PRG2.
CC   -!- PTM: C3b is rapidly split in two positions by factor I and a
CC       cofactor to form iC3b (inactivated C3b) and C3f which is released.
CC       Then iC3b is slowly cleaved (possibly by factor I) to form C3c and
CC       C3dg. Other proteases produce other fragments such as C3d or C3g.
CC   -!- POLYMORPHISM: There are two alleles: C3S (C3 slow), the most
CC       common allele in all races and C3F (C3 fast), relatively frequent
CC       in Caucasoids, less common in Black Americans, extremely rare in
CC       Orientals.
CC   -!- DISEASE: Defects in C3 are the cause of C3 deficiency
CC       [MIM:120700]. It can result in susceptibility to pyogenic
CC       infection.
CC   -!- SIMILARITY: Contains 1 anaphylatoxin-like domain.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; K02765; AAA85332.1; -; mRNA.
DR   EMBL; AY513239; AAR89906.1; -; Genomic_DNA.
DR   PIR; A94065; C3HU.
DR   PDB; 1C3D; X-ray; @=-.
DR   PDB; 1GHQ; X-ray; A=996-1300.
DR   GlycoSuiteDB; P01024; -.
DR   SWISS-2DPAGE; P01024; HUMAN.
DR   Siena-2DPAGE; P01024; -.
DR   Ensembl; ENSG00000125730; Homo sapiens.
DR   HGNC; HGNC:1318; C3.
DR   MIM; 120700; -.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   GO; GO:0006955; P:immune response; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR011626; A2M_comp.
DR   InterPro; IPR002890; A2M_N.
DR   InterPro; IPR011625; A2M_N_2.
DR   InterPro; IPR011627; A2M_receptor.
DR   InterPro; IPR000020; Anaphylatoxin.
DR   InterPro; IPR001840; Anaphylatoxn.
DR   InterPro; IPR001599; MacroglobInA2.
DR   InterPro; IPR001134; Netrin_C.
DR   Pfam; PF00207; A2M; 1.
DR   Pfam; PF07678; A2M_comp; 1.
DR   Pfam; PF01835; A2M_N; 1.
DR   Pfam; PF07703; A2M_N_2; 1.
DR   Pfam; PF07677; A2M_recep; 1.
DR   Pfam; PF01821; ANATO; 1.
DR   Pfam; PF01759; NTR; 1.
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DR   PRINTS; PR00004; ANAPHYLATOXN.
DR   ProDom; PD003264; Anaphylatoxin; 1.

  Query Match             100.0%;  Score 91;  DB 1;  Length 1663;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-06;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db       1217 KNRWEDPGKQLYNVEA 1232


RESULT 2
CO3_RAT
ID   CO3_RAT        STANDARD;      PRT;  1663 AA.
AC   P01026;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Complement C3 precursor [Contains: Complement C3 beta chain;
DE   Complement C3 alpha chain; C3a anaphylatoxin; Complement C3b alpha'
DE   chain].
GN   Name=C3;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Wistar; TISSUE=Liver;
RX   MEDLINE=90245672; PubMed=2336397;
RA   Misumi Y., Sohda M., Ikehara Y.;
RT   "Nucleotide and deduced amino acid sequence of rat complement C3.";
RL   Nucleic Acids Res. 18:2178-2178(1990).
RN   [2]
RP   PROTEIN SEQUENCE OF 671-748.
RX   MEDLINE=79062262; PubMed=309768;
RA   Jacobs J.W., Rubin J.S., Hugli T.E., Bogardt R.A. Jr., Mariz I.K.,
RA   Daniels J.S., Daughaday W.H., Bradshaw R.A.;
RT   "Purification, characterization, and amino acid sequence of rat
RT   anaphylatoxin (C3a).";
RL   Biochemistry 17:5031-5038(1978).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 1316-1595.
RX   MEDLINE=89380332; PubMed=2674144;
RA   Sundstrom S.A., Komm B.S., Ponce-De-Leon H., Yi Z., Teuscher C.,
RA   Lyttle C.R.;
RT   "Estrogen regulation of tissue-specific expression of complement C3.";
RL   J. Biol. Chem. 264:16941-16947(1989).
CC   -!- FUNCTION: C3 plays a central role in the activation of the
CC       complement system. Its processing by C3 convertase is the central
CC       reaction in both classical and alternative complement pathways.
CC       After activation C3b can bind covalently, via its reactive
CC       thiolester, to cell surface carbohydrates or immune aggregates.
CC   -!- FUNCTION: Derived from proteolytic degradation of complement C3,
CC       C3a anaphylatoxin is a mediator of local inflammatory process. It
CC       induces the contraction of smooth muscle, increases vascular
CC       permeability and causes histamine release from mast cells and
CC       basophilic leukocytes.
CC   -!- SUBUNIT: C3 precursor is first processed by the removal of 4 Arg
CC       residues, forming two chains, beta and alpha, linked by a
CC       disulfide bond. C3 convertase activates C3 by cleaving the alpha
CC       chain, releasing C3a anaphylatoxin and generating C3b (beta chain
CC       + alpha' chain).
CC   -!- SIMILARITY: Contains 1 anaphylatoxin-like domain.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X52477; CAA36716.1; -; mRNA.
DR   EMBL; M29866; AAA40837.1; ALT_SEQ; mRNA.
DR   PIR; S15764; C3RT.
DR   PDB; 1QQF; X-ray; A=1010-1286.
DR   PDB; 1QSJ; X-ray; A/B/C/D=1010-1286.
DR   RGD; 2232; C3.
DR   InterPro; IPR011626; A2M_comp.
DR   InterPro; IPR002890; A2M_N.
DR   InterPro; IPR011625; A2M_N_2.
DR   InterPro; IPR011627; A2M_receptor.
DR   InterPro; IPR000020; Anaphylatoxin.
DR   InterPro; IPR001840; Anaphylatoxn.
DR   InterPro; IPR001599; MacroglobInA2.
DR   InterPro; IPR001134; Netrin_C.
DR   Pfam; PF00207; A2M; 1.
DR   Pfam; PF07678; A2M_comp; 1.
DR   Pfam; PF01835; A2M_N; 1.
DR   Pfam; PF07703; A2M_N_2; 1.
DR   Pfam; PF07677; A2M_recep; 1.
DR   Pfam; PF01821; ANATO; 1.
DR   Pfam; PF01759; NTR; 1.
DR   PRINTS; PR00004; ANAPHYLATOXN.
DR   ProDom; PD003264; Anaphylatoxin; 1.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR   PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR   PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR   PROSITE; PS50189; NTR; 1.
KW   3D-structure; Complement alternate pathway; Complement pathway;
KW   Direct protein sequencing; Glycoprotein; Immune response;
KW   Inflammatory response; Innate immunity; Plasma; Signal;
KW   Thioester bond.
FT   SIGNAL       1     24
FT   CHAIN       25   1663       Complement C3.
FT   CHAIN       25    666       Complement C3 beta chain.
FT   CHAIN      671   1663       Complement C3 alpha chain.
FT   PEPTIDE    671    748       C3a anaphylatoxin.
FT   CHAIN      749   1663       Complement C3b alpha' chain.
FT   DOMAIN     693    728       Anaphylatoxin-like.
FT   DOMAIN    1518   1661       NTR.
FT   SITE       748    749       Cleavage (by C3 convertase).
FT   CARBOHYD   939    939       N-linked (GlcNAc. . .) (Probable).
FT   CARBOHYD  1617   1617       N-linked (GlcNAc. . .) (Probable).
FT   DISULFID   558    816       Interchain (between beta and alpha
FT                               chains) (By similarity).
FT   DISULFID   626    661       By similarity.
FT   DISULFID   693    720       By similarity.
FT   DISULFID   694    727       By similarity.
FT   DISULFID   707    728       By similarity.
FT   DISULFID   873   1513       By similarity.
FT   DISULFID  1101   1158       By similarity.
FT   DISULFID  1358   1489       By similarity.
FT   DISULFID  1389   1458       By similarity.
FT   DISULFID  1506   1511       By similarity.
FT   DISULFID  1518   1590       By similarity.
FT   DISULFID  1537   1661       By similarity.
FT   CROSSLNK  1010   1013       Isoglutamyl cysteine thioester (Cys-Gln).
FT   CONFLICT   721    722       LK -> KL (in Ref. 2).
FT   TURN      1011   1012
FT   HELIX     1013   1031
FT   TURN      1032   1032
FT   HELIX     1034   1037
FT   HELIX     1039   1041
FT   HELIX     1042   1057
FT   TURN      1058   1059
FT   STRAND    1060   1060
FT   TURN      1062   1063
FT   STRAND    1066   1066
FT   TURN      1070   1071
FT   HELIX     1076   1089
FT   TURN      1090   1092
FT   HELIX     1097   1111
FT   STRAND    1112   1112
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FT   TURN        1114   1115
FT   STRAND      1118   1118
FT   HELIX       1127   1134
FT   TURN        1137   1138
FT   HELIX       1139   1158
FT   TURN        1159   1161
FT   TURN        1163   1164
FT   HELIX       1165   1180
FT   TURN        1181   1182
FT   HELIX       1186   1198
FT   TURN        1199   1200
FT   TURN        1204   1205
FT   HELIX       1206   1213
FT   STRAND      1215   1215
FT   TURN        1216   1218
FT   STRAND      1219   1219
FT   TURN        1223   1224
FT   HELIX       1226   1242
FT   TURN        1243   1244
FT   TURN        1246   1247
FT   HELIX       1249   1258
FT   TURN        1263   1264
FT   TURN        1266   1267
FT   HELIX       1269   1285
SQ   SEQUENCE   1663 AA;  186460 MW;  2F87CCB143CDD4BC CRC64;

  Query Match             87.9%;  Score 80;  DB 1;  Length 1663;
  Best Local Similarity   81.2%;  Pred. No. 0.00023;
  Matches   13;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              :||||:||:|||||||
Db       1217 RNRWEEPGQQLYNVEA 1232


RESULT 3
CO3_RABIT
ID   CO3_RABIT      STANDARD;      PRT;   726 AA.
AC   P12247;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Complement C3 alpha chain (Fragment).
GN   Name=C3;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87006907; PubMed=3019881;
RA   Kusano M., Choi N.H., Tomita M., Yamamoto K., Migita S., Sekiya T.,
RA   Nishimura S.;
RT   "Nucleotide sequence of cDNA and derived amino acid sequence of rabbit
RT   complement component C3 alpha-chain.";
RL   Immunol. Invest. 15:365-378(1986).
CC   -!- FUNCTION: C3 plays a central role in the activation of the
CC       complement system. Its processing by C3 convertase is the central
CC       reaction in both classical and alternative complement pathways.
CC       After activation C3b can bind covalently, via its reactive
CC       thiolester, to cell surface carbohydrates or immune aggregates.
CC   -!- SUBUNIT: C3 precursor is first processed by the removal of 4 Arg
CC       residues, forming two chains, beta and alpha, linked by a
CC       disulfide bond. C3 convertase activates C3 by cleaving the alpha
CC       chain, releasing C3a anaphylatoxin and generating C3b (beta chain
CC       + alpha' chain).
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M32434; AAA31190.1; -; mRNA.
DR   PIR; A27602; A27602.
DR   HSSP; P01024; 1C3D.
DR   SMR; P12247; 58-362.
DR   InterPro; IPR011626; A2M_comp.
DR   InterPro; IPR011627; A2M_receptor.
DR   InterPro; IPR000020; Anaphylatoxin.
DR   InterPro; IPR001599; MacroglobInA2.
DR   InterPro; IPR001134; Netrin_C.
DR   Pfam; PF07678; A2M_comp; 1.
DR   Pfam; PF07677; A2M_recep; 1.
DR   Pfam; PF01759; NTR; 1.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR   PROSITE; PS01177; ANAPHYLATOXIN_1; PARTIAL.
DR   PROSITE; PS01178; ANAPHYLATOXIN_2; PARTIAL.
DR   PROSITE; PS50189; NTR; 1.
KW   Complement alternate pathway; Complement pathway; Glycoprotein;
KW   Immune response; Inflammatory response; Innate immunity; Plasma;
KW   Thioester bond.
FT   CHAIN        <1    726       Complement C3 alpha chain.
FT   DOMAIN      581    724       NTR.
FT   CARBOHYD      2      2       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    233    233       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    680    680       N-linked (GlcNAc. . .) (Potential).
FT   CROSSLNK     73     76       Isoglutamyl cysteine thioester (Cys-Gln).
FT   NON_TER       1      1
SQ   SEQUENCE   726 AA;  81844 MW;  F4B4C35D461300E9 CRC64;

  Query Match             86.8%;  Score 79;  DB 1;  Length 726;
  Best Local Similarity   81.2%;  Pred. No. 0.00013;
  Matches   13;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              |||||:||::||||||
Db        280 KNRWEEPGQRLYNVEA 295


RESULT 4
O46544_SHEEP
ID   O46544_SHEEP PRELIMINARY;      PRT;   349 AA.
AC   O46544;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Complement component C3 (Fragment).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=white alpine; TISSUE=Liver;
RX   MEDLINE=98309471; PubMed=9647256;
RA   Hein W.R., Dudler L., Marston W.L., Landsverk T., Young A.J.,
RA   Avila D.;
RT   "Ubiquitination and dimerization of complement receptor type 2 on
RT   sheep B cells.";
RL   J. Immunol. 161:458-466(1998).
DR   EMBL; AF038130; AAB92374.2; -; mRNA.
DR   HSSP; P01026; 1QQF.
DR   SMR; O46544; 19-322.
DR   GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR011626; A2M_comp.
DR   InterPro; IPR001599; MacroglobInA2.
DR   Pfam; PF07678; A2M_comp; 1.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
FT   NON_TER       1      1
FT   NON_TER     349    349
SQ   SEQUENCE   349 AA;  39679 MW;  70C2023E42ED5EE3 CRC64;
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  Query Match            84.6%;  Score 77;  DB 2;  Length 349;
  Best Local Similarity   81.2%;  Pred. No. 0.00013;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              |||||:| |:||||||
Db        241 KNRWEEPNKKLYNVEA 256


RESULT 5
Q29289_PIG
ID   Q29289_PIG  PRELIMINARY;      PRT;   154 AA.
AC   Q29289;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Complement C3 (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Small intestine;
RX   MEDLINE=96327607; PubMed=8672129; DOI=10.1007/s003359900153;
RA   Winteroe A.K., Fredholm M., Davies W.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library: analysis of 839 clones.";
RL   Mamm. Genome 7:509-517(1996).
DR   EMBL; F14640; CAA23173.1; -; mRNA.
DR   HSSP; P01026; 1QQF.
DR   SMR; Q29289; 8-91.
DR   InterPro; IPR011626; A2M_comp.
DR   Pfam; PF07678; A2M_comp; 1.
FT   NON_TER       1      1
FT   NON_TER     154    154
SQ   SEQUENCE   154 AA;  17440 MW;  6DC7661C1253ED45 CRC64;

  Query Match            83.5%;  Score 76;  DB 2;  Length 154;
  Best Local Similarity   75.0%;  Pred. No. 7.8e-05;
  Matches   12;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              :||||:||::||||||
Db         10 RNRWEEPGQKLYNVEA 25


RESULT 6
Q9Z115_MESAU
ID   Q9Z115_MESAU PRELIMINARY;      PRT;   310 AA.
AC   Q9Z115;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Complement C3 (Fragment).
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Cricetinae; Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yamamoto K., Inoue N., Sakiyama H.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB024425; BAA75923.1; -; mRNA.
DR   HSSP; P01026; 1QQF.
DR   SMR; Q9Z115; 18-293.
DR   GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR011626; A2M_comp.
DR   InterPro; IPR001599; MacrogloblnA2.
DR   Pfam; PF07678; A2M_comp; 1.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
FT   NON_TER       1      1
FT   NON_TER     310    310
SQ   SEQUENCE   310 AA;  34779 MW;  11ED3BEEF82D327D CRC64;

  Query Match            83.5%;  Score 76;  DB 2;  Length 310;
  Best Local Similarity   75.0%;  Pred. No. 0.00017;
  Matches   12;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              :||||:||::||||||
Db        224 RNRWEEPGQKLYNVEA 239


RESULT 7
Q693V9_BOVIN
ID   Q693V9_BOVIN PRELIMINARY;      PRT;   303 AA.
AC   Q693V9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Complement component C3d (Fragment).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hodgins D., Firth M., Pei Y., Yoo D., Shewen P.;
RT   "Cloning, Sequencing and Analysis of the C3d Fragment of Bovine
RT   Complement Component 3.";
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY630404; AAT76518.1; -; mRNA.
DR   SMR; Q693V9; 1-298.
DR   GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
DR   InterPro; IPR011626; A2M_comp.
DR   InterPro; IPR001599; MacrogloblnA2.
DR   Pfam; PF07678; A2M_comp; 1.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
FT   NON_TER       1      1
FT   NON_TER     303    303
SQ   SEQUENCE   303 AA;  34443 MW;  2F3A15020CEA3797 CRC64;

  Query Match            80.2%;  Score 73;  DB 2;  Length 303;
  Best Local Similarity   75.0%;  Pred. No. 0.00056;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              |||||:| ::||||||
Db        216 KNRWEEPNQKLYNVEA 231


RESULT 8
CO3_MOUSE
ID   CO3_MOUSE      STANDARD;      PRT;  1663 AA.
AC   P01027; Q61370;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Complement C3 precursor (HSE-MSF) [Contains: Complement C3 beta chain;
DE   Complement C3 alpha chain; C3a anaphylatoxin; Complement C3b alpha'
DE   chain; Complement C3c fragment; Complement C3dg fragment; Complement
DE   C3g fragment; Complement C3d fragment; Complement C3, isoform Short;
DE   C3f fragment].
GN   Name=C3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RX   MEDLINE=85038854; PubMed=6208565;
```

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RA   Fey G.H., Lundwall A., Wetsel R.A., Tack B.F., de Bruijn M.H.L.,
RA   Domdey H.;
RT   "Nucleotide sequence of complementary DNA and derived amino acid
RT   sequence of murine complement protein C3.";
RL   Philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:333-344(1984).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 1-724 (ISOFORM LONG).
RX   MEDLINE=85054818; PubMed=6548745;
RA   Lundwall A., Wetsel R.A., Domdey H., Tack B.F., Fey G.H.;
RT   "Structure of murine complement component C3. I. Nucleotide sequence
RT   of cloned complementary and genomic DNA coding for the beta chain.";
RL   J. Biol. Chem. 259:13851-13856(1984).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 25-1663 (ISOFORM LONG).
RX   MEDLINE=85113177; PubMed=2578664;
RA   Sottrup-Jensen L., Stepanik T.M., Kristensen T., Lonblad P.B.,
RA   Jones C.M., Wierzbicki D.M., Magnusson S., Domdey H., Wetsel R.A.,
RA   Lundwall A., Tack B.F., Fey G.H.;
RT   "Common evolutionary origin of alpha 2-macroglobulin and complement
RT   components C3 and C4.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:9-13(1985).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 25-240 (ISOFORM LONG).
RX   MEDLINE=84045280; PubMed=6356427; DOI=10.1007/BF00205869;
RA   Fey G., Domdey H., Wiebauer K., Whitehead A.S., Odink K.;
RT   "Structure and expression of the C3 gene.";
RL   Springer Semin. Immunopathol. 6:119-147(1983).
RN   [5]
RP   NUCLEOTIDE SEQUENCE OF 671-1663 (ISOFORM LONG).
RX   MEDLINE=85054819; PubMed=6094532;
RA   Wetsel R.A., Lundwall A., Davidson F., Gibson T., Tack B.F., Fey G.H.;
RT   "Structure of murine complement component C3. II. Nucleotide sequence
RT   of cloned complementary DNA coding for the alpha chain.";
RL   J. Biol. Chem. 259:13857-13862(1984).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 671-748.
RX   MEDLINE=83117730; PubMed=6961437;
RA   Domdey H., Wiebauer K., Kazmaier M., Mueller V., Odink K., Fey G.H.;
RT   "Characterization of the mRNA and cloned cDNA specifying the third
RT   component of mouse complement.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:7619-7623(1982).
RN   [7]
RP   NUCLEOTIDE SEQUENCE OF 658-761.
RX   MEDLINE=84201365; PubMed=6609661;
RA   Fey G.H., Wiebauer K., Domdey H.;
RT   "Amino acid sequences of mouse complement C3 derived from nucleotide
RT   sequences of cloned cDNA.";
RL   Ann. N. Y. Acad. Sci. 421:307-312(1983).
RN   [8]
RP   NUCLEOTIDE SEQUENCE OF 1-34.
RX   MEDLINE=83117622; PubMed=6985486;
RA   Wiebauer K., Domdey H., Diggelmann H., Fey G.;
RT   "Isolation and analysis of genomic DNA clones encoding the third
RT   component of mouse complement.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:7077-7081(1982).
RN   [9]
RP   PROTEIN SEQUENCE OF 25-41 AND 749-760.
RX   MEDLINE=93373334; PubMed=8364938;
RA   Hamada J.-I., Cavanaugh P.G., Miki K., Nicolson G.L.;
RT   "A paracrine migration-stimulating factor for metastatic tumor cells
RT   secreted by mouse hepatic sinusoidal endothelial cells: identification
RT   as complement component C3b.";
RL   Cancer Res. 53:4418-4423(1993).
RN   [10]
RP   PROTEIN SEQUENCE OF 25-31 AND 671-680.
RX   MEDLINE=91293304; PubMed=2065778; DOI=10.1016/0014-5793(91)80715-F;
RA   Sato T., Hong M.H., Jin C.H., Ishimi Y., Udagawa N., Shinki T.,
RA   Abe E., Suda T.;
RT   "The specific production of the third component of complement by
RT   osteoblastic cells treated with 1 alpha,25-dihydroxyvitamin D3.";
RL   FEBS Lett. 285:21-24(1991).
RN   [11]
RP   ALTERNATIVE INITIATION.
RX   MEDLINE=95053742; PubMed=7964485; DOI=10.1084/jem.180.6.2079;
RA   Cahen-Kramer Y., Martensson I.L., Melchers F.;
RT   "The structure of an alternate form of complement C3 that displays
RT   costimulatory growth factor activity for B lymphocytes.";
RL   J. Exp. Med. 180:2079-2088(1994).
CC   -!- FUNCTION: C3 plays a central role in the activation of the
CC       complement system. Its processing by C3 convertase is the central
CC       reaction in both classical and alternative complement pathways.
CC       After activation C3b can bind covalently, via its reactive
CC       thiolester, to cell surface carbohydrates or immune aggregates.
CC   -!- FUNCTION: Derived from proteolytic degradation of complement C3,
CC       C3a anaphylatoxin is a mediator of local inflammatory process. It
CC       induces the contraction of smooth muscle, increases vascular
CC       permeability and causes histamine release from mast cells and
CC       basophilic leukocytes. The short isoform has B-cell stimulatory
CC       activity.
CC   -!- SUBUNIT: C3 precursor is first processed by the removal of 4 Arg
CC       residues, forming two chains, beta and alpha, linked by a
CC       disulfide bond. C3 convertase activates C3 by cleaving the alpha
CC       chain, releasing C3a anaphylatoxin and generating C3b (beta chain
CC       + alpha' chain).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative initiation;
CC         Comment=2 isoforms, Long (shown here) and Short, are produced by
CC         alternative initiation;
CC   -!- PTM: C3b is rapidly split in two positions by factor I and a
CC       cofactor to form iC3b (inactivated C3b) and C3f which is released.
CC       Then iC3b is slowly cleaved (possibly by factor I) to form C3c and
CC       C3dg. Other proteases produce other fragments such as C3d or C3g.
CC   -!- SIMILARITY: Contains 1 anaphylatoxin-like domain.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; K02782; AAC42013.1; -; mRNA.
DR   EMBL; J00369; AAA37336.1; -; Genomic_DNA.
DR   EMBL; J00367; AAA37336.1; JOINED; Genomic_DNA.
DR   EMBL; M35659; AAA37339.1; -; mRNA.
DR   EMBL; M33032; AAA37378.1; -; mRNA.
DR   EMBL; Z37998; CAA86099.2; -; Genomic_DNA.
DR   PIR; A92459; C3MS.
DR   HSSP; P01026; 1QQF.
DR   SMR; P01027; 1011-1286.
DR   Ensembl; ENSMUSG00000024164; Mus musculus.
DR   MGI; MGI:88227; C3.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0050766; P:positive regulation of phagocytosis; IMP.
DR   GO; GO:0001798; P:positive regulation of type IIa hypersensit. . .; IMP.
DR   InterPro; IPR011626; A2M_comp.
DR   InterPro; IPR002890; A2M_N.
DR   InterPro; IPR011625; A2M_N_2.
DR   InterPro; IPR011627; A2M_receptor.
DR   InterPro; IPR000020; Anaphylatoxin.
DR   InterPro; IPR001840; Anaphylatoxn.
DR   InterPro; IPR001599; MacroglobInA2.
DR   InterPro; IPR001134; Netrin_C.
DR   Pfam; PF00207; A2M; 1.
DR   Pfam; PF07678; A2M_comp; 1.
DR   Pfam; PF01835; A2M_N; 1.
DR   Pfam; PF07703; A2M_N_2; 1.
DR   Pfam; PF07677; A2M_recep; 1.
DR   Pfam; PF01821; ANATO; 1.
DR   Pfam; PF01759; NTR; 1.
DR   PRINTS; PR00004; ANAPHYLATOXN.
DR   ProDom; PD003264; Anaphylatoxin; 1.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR   PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR   PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
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DR   PROSITE; PS50189; NTR; 1.
KW   Alternative initiation; Complement alternate pathway;
KW   Complement pathway; Direct protein sequencing; Glycoprotein;
KW   Immune response; Inflammatory response; Innate immunity; Plasma;
KW   Signal; Thioester bond.
FT   SIGNAL        1     24
FT   CHAIN        25   1663       Complement C3, isoform Long.
FT   CHAIN        25    666       Complement C3 beta chain.
FT   CHAIN       671   1663       Complement C3 alpha chain.
FT   PEPTIDE     671    748       C3a anaphylatoxin.
FT   CHAIN       749   1663       Complement C3b alpha' chain.
FT   CHAIN       749    954       Complement C3c fragment.
FT   CHAIN       955   1303       Complement C3dg fragment.
FT   CHAIN       955   1001       Complement C3g fragment.
FT   CHAIN      1002   1303       Complement C3d fragment.
FT   CHAIN      1129   1663       Complement C3, isoform Short.
FT   INIT_MET   1129   1129       For isoform Short.
FT   PEPTIDE    1304   1320       C3f fragment.
FT   DOMAIN      693    728       Anaphylatoxin-like.
FT   DOMAIN     1518   1661       NTR.
FT   SITE        748    749       Cleavage (by C3 convertase).
FT   SITE       1303   1304       Cleavage (by factor I).
FT   SITE       1320   1321       Cleavage (by factor I).
FT   CARBOHYD    939    939       N-linked (GlcNAc. . .).
FT   CARBOHYD   1617   1617       N-linked (GlcNAc. . .).
FT   DISULFID    559    816       Interchain (between beta and alpha
FT                                chains) (By similarity).
FT   DISULFID    626    661       By similarity.
FT   DISULFID    693    720       By similarity.
FT   DISULFID    694    727       By similarity.
FT   DISULFID    707    728       By similarity.
FT   DISULFID    873   1513       By similarity.
FT   DISULFID   1101   1158       By similarity.
FT   DISULFID   1358   1489       By similarity.
FT   DISULFID   1389   1458       By similarity.

  Query Match             80.2%;  Score 73;  DB 1;  Length 1663;
  Best Local Similarity   75.0%;  Pred. No. 0.0038;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              :||||:| :|||||||
Db       1217 RNRWEEPDQQLYNVEA 1232


RESULT 9
Q80XP1_MOUSE
ID   Q80XP1_MOUSE PRELIMINARY;      PRT;  1663 AA.
AC   Q80XP1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Complement component 3.
GN   Name=C3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC043338; AAH43338.1; -; mRNA.
DR   HSSP; P01026; 1QQF.
DR   SMR; Q80XP1; 1011-1286.
DR   MGI; MGI:88227; C3.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0050766; P:positive regulation of phagocytosis; IMP.
DR   GO; GO:0001798; P:positive regulation of type IIa hypersensit. . .; IMP.
DR   InterPro; IPR011626; A2M_comp.
DR   InterPro; IPR002890; A2M_N.
DR   InterPro; IPR011625; A2M_N_2.
DR   InterPro; IPR011627; A2M_receptor.
DR   InterPro; IPR000020; Anaphylatoxin.
DR   InterPro; IPR001840; Anaphylatoxn.
DR   InterPro; IPR001599; MacroglobInA2.
DR   InterPro; IPR001134; Netrin_C.
DR   Pfam; PF00207; A2M; 1.
DR   Pfam; PF07678; A2M_comp; 1.
DR   Pfam; PF01835; A2M_N; 1.
DR   Pfam; PF07703; A2M_N_2; 1.
DR   Pfam; PF07677; A2M_recep; 1.
DR   Pfam; PF01821; ANATO; 1.
DR   Pfam; PF01759; NTR; 1.
DR   PRINTS; PR00004; ANAPHYLATOXN.
DR   ProDom; PD003264; Anaphylatoxin; 1.
DR   SMART; SM00104; ANATO; 1.
DR   SMART; SM00643; C345C; 1.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR   PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR   PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR   PROSITE; PS50189; NTR; 1.
SQ   SEQUENCE   1663 AA;  186483 MW;  7E5546CC7C314779 CRC64;

  Query Match             80.2%;  Score 73;  DB 2;  Length 1663;
  Best Local Similarity   75.0%;  Pred. No. 0.0038;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              :||||:| :|||||||
Db       1217 RNRWEEPDQQLYNVEA 1232


RESULT 10
Q9GKP1_PIG
ID   Q9GKP1_PIG  PRELIMINARY;      PRT;  1661 AA.
AC   Q9GKP1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Complement component C3 (Complement C3).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
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RX   MEDLINE=21313047; PubMed=11419349;
RA   Wimmers K., Mekchay S., Ponsuksili S., Hardge T., Yerle M.,
RA   Schellander K.;
RT   "Polymorphic sites in exon 15 and 30 of the porcine C3 gene.";
RL   Anim. Genet. 32:46-47(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Wimmers K., Ponsuksili S., Schmoll F., Schellander K.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=22444329; PubMed=12557058;
RA   Wimmers K., Mekchay S., Schellander K., Ponsuksili S.;
RT   "Molecular characterization of the pig C3 gene and its association
RT   with complement activity.";
RL   Immunogenetics 54:714-724(2003).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Wimmers K., Mekchay S., Schellander K., Ponsuksili S.;
RT   "Molecular characterization of the pig C3 gene and its association
RT   with complement activity.";
RL   (er) Immunogenetics.
DR   EMBL; AF154933; AAG40565.1; -; mRNA.
DR   EMBL; AJ494748; CAD38823.2; -; Genomic_DNA.
DR   HSSP; P01026; 1QQF.
DR   SMR; Q9GKP1; 993-1297.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
DR   GO; GO:0006958; P:complement activation, classical pathway; IEA.
DR   GO; GO:0006954; P:inflammatory response; IEA.
DR   InterPro; IPR011626; A2M_comp.
DR   InterPro; IPR002890; A2M_N.
DR   InterPro; IPR011625; A2M_N_2.
DR   InterPro; IPR011627; A2M_receptor.
DR   InterPro; IPR000020; Anaphylatoxin.
DR   InterPro; IPR001840; Anaphylatoxn.
DR   InterPro; IPR001599; MacroglobInA2.
DR   InterPro; IPR001134; Netrin_C.
DR   Pfam; PF00207; A2M; 1.
DR   Pfam; PF07678; A2M_comp; 1.
DR   Pfam; PF01835; A2M_N; 1.
DR   Pfam; PF07703; A2M_N_2; 1.
DR   Pfam; PF07677; A2M_recep; 1.
DR   Pfam; PF01821; ANATO; 1.
DR   Pfam; PF01759; NTR; 1.
DR   PRINTS; PR00004; ANAPHYLATOXN.
DR   ProDom; PD003264; Anaphylatoxin; 1.
DR   SMART; SM00104; ANATO; 1.
DR   SMART; SM00643; C345C; 1.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR   PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR   PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR   PROSITE; PS50189; NTR; 1.
SQ   SEQUENCE   1661 AA;  186805 MW;  4899D0914BE3310C CRC64;

  Query Match             78.0%;  Score 71;  DB 2;  Length 1661;
  Best Local Similarity   68.8%;  Pred. No. 0.0084;
  Matches   11;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              :||||:||::|:||||
Db       1215 RNRWEEPGQKLHNVEA 1230


RESULT 11
CO3_CAVPO
ID   CO3_CAVPO      STANDARD;      PRT;  1666 AA.
AC   P12387;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Complement C3 precursor [Contains: Complement C3 beta chain;
DE   Complement C3 alpha chain; C3a anaphylatoxin; Complement C3b alpha'
DE   chain; Complement C3d fragment].
GN   Name=C3;
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC   Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Hartley; TISSUE=Liver;
RX   MEDLINE=90307998; PubMed=1973176;
RA   Auerbach H.S., Burger R., Dodds A., Colten H.R.;
RT   "Molecular basis of complement C3 deficiency in guinea pigs.";
RL   J. Clin. Invest. 86:96-106(1990).
RN   [2]
RP   PROTEIN SEQUENCE OF 23-38.
RC   TISSUE=Macrophage;
RX   MEDLINE=82075767; PubMed=6458605;
RA   Goldberger G., Thomas M.L., Tack B.F., Williams J., Colten H.R.,
RA   Abraham G.N.;
RT   "NH2-terminal structure and cleavage of guinea pig pro-C3, the
RT   precursor of the third complement component.";
RL   J. Biol. Chem. 256:12617-12619(1981).
RN   [3]
RP   PROTEIN SEQUENCE OF 23-38; 676-687 AND 993-1032, AND THIOESTER BOND.
RC   TISSUE=Plasma;
RX   MEDLINE=83178889; PubMed=6838833;
RA   Thomas M.L., Tack B.F.;
RT   "Identification and alignment of a thiol ester site in the third
RT   component of guinea pig complement.";
RL   Biochemistry 22:942-947(1983).
RN   [4]
RP   PROTEIN SEQUENCE OF 676-753.
RX   MEDLINE=89113342; PubMed=3064079;
RA   Gerard N.P., Lively M.O., Gerard C.;
RT   "Amino acid sequence of guinea pig C3a anaphylatoxin.";
RL   Protein Seq. Data Anal. 1:473-478(1988).
CC   -!- FUNCTION: C3 plays a central role in the activation of the
CC       complement system. Its processing by C3 convertase is the central
CC       reaction in both classical and alternative complement pathways.
CC       After activation C3b can bind covalently, via its reactive
CC       thiolester, to cell surface carbohydrates or immune aggregates.
CC   -!- FUNCTION: Derived from proteolytic degradation of complement C3,
CC       C3a anaphylatoxin is a mediator of local inflammatory process. It
CC       induces the contraction of smooth muscle, increases vascular
CC       permeability and causes histamine release from mast cells and
CC       basophilic leukocytes.
CC   -!- PTM: First processed by the removal of 4 Arg residues by furin-
CC       type protease, forming two chains, alpha and gamma/beta precursor,
CC       linked by a disulfide bond. C3 convertase activates C3 by cleaving
CC       the alpha chain, releasing C3a anaphylatoxin and generating C3b
CC       (beta chain + alpha' chain). Processing by elastase produces the
CC       C3d fragment.
CC   -!- SIMILARITY: Contains 1 anaphylatoxin-like domain.
CC   -!- SIMILARITY: Contains 1 NTR domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M34054; AAA37038.1; -; mRNA.
DR   PIR; A37156; C3GP.
DR   HSSP; P01026; 1QQF.
DR   InterPro; IPR011626; A2M_comp.
DR   InterPro; IPR002890; A2M_N.
DR   InterPro; IPR011625; A2M_N_2.
DR   InterPro; IPR011627; A2M_receptor.
DR   InterPro; IPR000020; Anaphylatoxin.
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DR   InterPro; IPR001840; Anaphylatoxn.
DR   InterPro; IPR001599; MacrogloblnA2.
DR   InterPro; IPR001134; Netrin_C.
DR   Pfam; PF00207; A2M; 1.
DR   Pfam; PF07678; A2M_comp; 1.
DR   Pfam; PF01835; A2M_N; 1.
DR   Pfam; PF07703; A2M_N_2; 1.
DR   Pfam; PF07677; A2M_recep; 1.
DR   Pfam; PF01821; ANATO; 1.
DR   Pfam; PF01759; NTR; 1.
DR   PRINTS; PR00004; ANAPHYLATOXN.
DR   ProDom; PD003264; Anaphylatoxin; 1.
DR   PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR   PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR   PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR   PROSITE; PS50189; NTR; 1.
KW   Complement alternate pathway; Complement pathway;
KW   Direct protein sequencing; Glycoprotein; Immune response;
KW   Inflammatory response; Innate immunity; Plasma; Signal;
KW   Thioester bond.
FT   SIGNAL        1     22
FT   CHAIN        23   1666       Complement C3.
FT   CHAIN        23    671       Complement C3 beta chain.
FT   CHAIN       676   1666       Complement C3 alpha chain.
FT   PEPTIDE     676    753       C3a anaphylatoxin.
FT   CHAIN       754   1666       Complement C3b alpha' chain.
FT   CHAIN       993   1666       Complement C3d fragment.
FT   DOMAIN      698    733       Anaphylatoxin-like.
FT   DOMAIN     1522   1664       NTR.
FT   COMPBIAS    672    675       Poly-Arg.
FT   COMPBIAS   1242   1248       Poly-Leu.
FT   SITE        753    754       Cleavage (by C3 convertase).
FT   SITE        992    993       Cleavage (by elastase).
FT   CARBOHYD    944    944       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   1620   1620       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    557    821       Interchain (between beta and alpha
FT                                chains) (By similarity).
FT   DISULFID    630    666       By similarity.
FT   DISULFID    698    725       By similarity.
FT   DISULFID    699    732       By similarity.
FT   DISULFID    712    733       By similarity.
FT   DISULFID    878   1517       By similarity.
FT   DISULFID   1106   1163       By similarity.
FT   DISULFID   1363   1493       By similarity.
FT   DISULFID   1394   1462       By similarity.
FT   DISULFID   1510   1515       By similarity.
FT   DISULFID   1522   1593       By similarity.
FT   DISULFID   1540   1664       By similarity.
FT   DISULFID   1640   1649       By similarity.
FT   CROSSLNK   1015   1018       Isoglutamyl cysteine thioester (Cys-Gln).
FT   CONFLICT    731    731       D -> N (in Ref. 4).
FT   CONFLICT   1018   1018       Q -> E (in Ref. 3).
SQ   SEQUENCE   1666 AA;  186488 MW;  1C1F1219944AFD49 CRC64;

  Query Match             63.7%;  Score 58;  DB 1;  Length 1666;
  Best Local Similarity   62.5%;  Pred. No. 1.5;
  Matches   10;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              |||||:  ::||:|||
Db       1222 KNRWEEARQKLYSVEA 1237


RESULT 12
R1_ARATH
ID   R1_ARATH       STANDARD;      PRT;  1399 AA.
AC   Q9SAC6; Q93VD0; Q940Z0; Q9FPP2;
DT   01-FEB-2005 (Rel. 46, Created)
DT   01-FEB-2005 (Rel. 46, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Alpha-glucan water dikinase, chloroplast precursor (EC 2.7.9.4)
DE   (Starch-related R1 protein) (Starch excess protein 1).
GN   Name=SEX1; Synonyms=R1; OrderedLocusNames=At1g10760;
GN   ORFNames=T16B5.10;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, SUBCELLULAR LOCATION,
RP   DEVELOPMENTAL STAGE, AND MUTAGENESIS OF GLY-1268.
RX   MEDLINE=21380420; PubMed=11487701; DOI=10.1105/tpc.13.8.1907;
RA   Yu T.-S., Kofler H., Haeusler R.E., Hille D., Fluegge U.-I.,
RA   Zeeman S.C., Smith A.M., Kossmann J., Lloyd J., Ritte G., Steup M.,
RA   Lue W.-L., Chen J., Weber A.;
RT   "The Arabidopsis sex1 mutant is defective in the R1 protein, a general
RT   regulator of starch degradation in plants, and not in the chloroplast
RT   hexose transporter.";
RL   Plant Cell 13:1907-1918(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=cv. Columbia;
RX   MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
RA   Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA   White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA   Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA   Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA   Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA   Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA   Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA   Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA   Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA   Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA   Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA   Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA   Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA   Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA   Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA   Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT   "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:816-820(2000).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1220-1399.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA   Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA   Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA   Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA   Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA   Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA   Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA   Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA   Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA   Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA   Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA   Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA   Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT   "Empirical analysis of transcriptional activity in the Arabidopsis
RT   genome.";
RL   Science 302:842-846(2003).
CC   -!- FUNCTION: Mediates the incorporation of phosphate into starch-like
CC       alpha-glucan. Acts as an overall regulator of starch mobilization.
CC       Required for starch degradation, suggesting that the phosphate
CC       content of starch regulates its degrability.
CC   -!- CATALYTIC ACTIVITY: ATP + alpha-glucan + H(2)O = AMP + phospho-
CC       alpha-glucan + phosphate.
CC   -!- COFACTOR: Magnesium (By similarity).
CC   -!- SUBCELLULAR LOCATION: Chloroplast; starch granules.
CC   -!- DEVELOPMENTAL STAGE: The level of protein does not vary in a
CC       circadian rythm and is stable throughout day and night (at protein
CC       level).
CC   -!- SIMILARITY: Belongs to the PEP-utilizing enzyme family.
CC   -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC       gene model prediction.
```

```
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AF312027; AAG47821.1; -; mRNA.
DR   EMBL; AC007354; AAD31337.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; AF372893; AAK49609.1; ALT_INIT; mRNA.
DR   EMBL; AY052349; AAK96541.1; ALT_INIT; mRNA.
DR   EMBL; AY057722; AAL15352.1; -; mRNA.
DR   PIR; B86241; B86241.
DR   InterPro; IPR008279; PEP_mobile.
DR   InterPro; IPR000121; PEP_utilizers.
DR   InterPro; IPR002192; PPDK_PEP_bd.
DR   Pfam; PF01326; PPDK_N; 1.
DR   PROSITE; PS00742; PEP_ENZYMES_2; FALSE_NEG.
DR   PROSITE; PS00370; PEP_ENZYMES_PHOS_SITE; FALSE_NEG.
KW   ATP-binding; Carbohydrate metabolism; Chloroplast; Kinase;
KW   Nucleotide-binding; Phosphorylation; Transferase; Transit peptide.
FT   TRANSIT       1     75       Chloroplast (By similarity).
FT   CHAIN        76   1399       Alpha-glucan water dikinase.
FT   ACT_SITE   1004   1004       Tele-phosphohistidine intermediate (By
FT                                similarity).
FT   MOD_RES    1004   1004       Phosphohistidine (By similarity).
FT   MUTAGEN    1268   1268       G->E: In sex1-1; induces an excess of
FT                                starch in leaves after a long period of
FT                                darkness.
SQ   SEQUENCE   1399 AA;  156582 MW;  1FE9285376B479EB CRC64;

  Query Match             57.1%;  Score 52;  DB 1;  Length 1399;
  Best Local Similarity   69.2%;  Pred. No. 14;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 RWEDPGKQLYNVE 15
              |||  |||:|| |
Db        223 RWERKGKQMYNPE 235


RESULT 13
Q9SGX4_ARATH
ID   Q9SGX4_ARATH PRELIMINARY;      PRT;  1540 AA.
AC   Q9SGX4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   F20B24.19.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA   Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA   Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA   Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA   Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA   Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA   Ecker J.R.;
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA   Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,
RA   Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA   Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
RA   Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA   Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
RA   Ecker J.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA   Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,
RA   Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA   Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
RA   Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA   Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
RA   Ecker J.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC009398; AAF17665.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004857; F:enzyme inhibitor activity; IEA.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0030599; F:pectinesterase activity; IEA.
DR   GO; GO:0016310; P:phosphorylation; IEA.
DR   InterPro; IPR007186; PMEI.
DR   InterPro; IPR006501; PME_inhib.
DR   InterPro; IPR002192; PPDK_N_term.
DR   Pfam; PF04043; PMEI; 1.
DR   Pfam; PF01326; PPDK_N; 1.
DR   TIGRFAMs; TIGR01614; PME_inhib; 1.
SQ   SEQUENCE   1540 AA;  172061 MW;  241B1433F0A2E79E CRC64;

  Query Match             57.1%;  Score 52;  DB 2;  Length 1540;
  Best Local Similarity   69.2%;  Pred. No. 16;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 RWEDPGKQLYNVE 15
              |||  |||:|| |
Db        357 RWERKGKQMYNPE 369


RESULT 14
Q57UI3_9TRYP
ID   Q57UI3_9TRYP PRELIMINARY;      PRT;  1188 AA.
AC   Q57UI3;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=Tb927.8.5110;
OS   Trypanosoma brucei.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX   NCBI_TaxID=5691;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=GUTat10.1;
RA   Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA   Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA   Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA   Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA   Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC159451; AAX70748.1; -; Genomic_DNA.
DR   InterPro; IPR001611; LRR.
DR   Pfam; PF00560; LRR_1; 1.
DR   PRINTS; PR00019; LEURICHRPT.
KW   Hypothetical protein; Leucine-rich repeat; Repeat.
SQ   SEQUENCE   1188 AA;  127078 MW;  08F9C6E39087B914 CRC64;

  Query Match             56.0%;  Score 51;  DB 2;  Length 1188;
  Best Local Similarity   69.2%;  Pred. No. 17;
  Matches    9;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 WEDPGKQLYNVEA 16
              ||||||:  :|||
Db        778 WEDPGKEDQDVEA 790


RESULT 15
Q9MXA7_BARIN
ID   Q9MXA7_BARIN PRELIMINARY;      PRT;    92 AA.
```

```
AC   Q9MXA7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MHC class I antigen (Fragment).
GN   Name=Bain-UA*L13;
OS   Barbus intermedius (Lake tana barbels).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Barbus.
OX   NCBI_TaxID=40831;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kruiswijk C.P., Stet R.J.M.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ007897; CAB97341.1; -; Genomic_DNA.
DR   HSSP; P01897; 1LDP.
DR   GO; GO:0042612; C:MHC class I protein complex; IEA.
DR   GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR   GO; GO:0019882; P:antigen presentation; IEA.
DR   InterPro; IPR001039; MHC_I_alpha_A1A2.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
FT   NON_TER       1      1
FT   NON_TER      92     92
SQ   SEQUENCE   92 AA;  10463 MW;  A1D08F3030F9E144 CRC64;

  Query Match             54.9%;  Score 50;  DB 2;  Length 92;
  Best Local Similarity   50.0%;  Pred. No. 1.5;
  Matches    8;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||:|:  | |: ||:|
Db         53 KNKWDSTGAQINNVKA 68


Search completed: May 15, 2006, 16:16:15
Job time : 231 secs
```

OM protein - protein search, using sw model

Run on: May 15, 2006, 16:28:51 ; Search time 180 Seconds
(without alignments)
39.056 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 19975

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	100.0	16	4	AAB92360	Aab92360 Miscellan
2	91	100.0	16	6	ABP58217	Abp58217 Immunosti
3	91	100.0	16	8	ADS17594	Ads17594 Peptide d
4	91	100.0	16	9	ADV24825	Adv24825 CR2-bindi
5	38	41.8	16	2	AAW32826	Aaw32826 HIV-1 CDC
6	37	40.7	16	1	AAP82479	Aap82479 Peptide c
7	37	40.7	16	2	AAR24424	Aar24424 Sequence
8	37	40.7	16	2	AAR85369	Aar85369 HTLV-IIIB
9	37	40.7	16	2	AAW07391	Aaw07391 HIV-1 CD4
10	37	40.7	16	2	AAW10345	Aaw10345 HIV epito
11	37	40.7	16	2	AAW16512	Aaw16512 HTLV-IIIB
12	37	40.7	16	2	AAW32824	Aaw32824 HIV-1 SC
13	37	40.7	16	2	AAW16535	Aaw16535 HIV-1 BH1
14	37	40.7	16	2	AAW32825	Aaw32825 HIV-1 SF2
15	37	40.7	16	2	AAW32822	Aaw32822 HIV-1 BRU
16	37	40.7	16	2	AAW32823	Aaw32823 HIV-1 MN
17	37	40.7	16	2	AAW32828	Aaw32828 HIV-1 RF
18	37	40.7	16	2	AAW53140	Aaw53140 HIV gp160
19	37	40.7	16	2	AAW85381	Aaw85381 Helper T-
20	37	40.7	16	2	AAW76982	Aaw76982 Fusion im
21	37	40.7	16	2	AAW54937	Aaw54937 HIV gp120
22	37	40.7	16	2	AAY04046	Aay04046 Covalentl
23	37	40.7	16	3	AAY73159	Aay73159 HIV-deriv
24	37	40.7	16	4	AAB49073	Aab49073 HIV gp120
25	37	40.7	16	4	AAB46174	Aab46174 HIV gp120
26	37	40.7	16	4	AAU12518	Aau12518 Human HIV
27	37	40.7	16	4	AAU12526	Aau12526 Human HIV
28	37	40.7	16	4	AAU12495	Aau12495 Human HIV
29	37	40.7	16	4	AAU12540	Aau12540 Human HIV
30	37	40.7	16	4	ABP25338	Abp25338 HTL cadid
31	37	40.7	16	4	ABP25261	Abp25261 HIV HLA-D
32	37	40.7	16	4	ABP25382	Abp25382 HIV-1 epi
33	37	40.7	16	5	AAM49301	Aam49301 CD4 pepti
34	37	40.7	16	5	AAE20151	Aae20151 Human imm
35	37	40.7	16	6	ABG72720	Abg72720 HIV-1 gp1
36	37	40.7	16	6	ABU87175	Abu87175 HIV T cel
37	37	40.7	16	7	ADA49515	Ada49515 Multi-epi
38	37	40.7	16	7	ADC09978	Adc09978 HIV gp120
39	37	40.7	16	7	ADW36356	Adw36356 HLA bindi
40	37	40.7	16	7	ADW36078	Adw36078 HLA bindi
41	37	40.7	16	7	ADW35909	Adw35909 HLA bindi
42	37	40.7	16	7	ADW33657	Adw33657 HLA bindi
43	37	40.7	16	7	ADW34890	Adw34890 HLA bindi
44	37	40.7	16	8	ADO24193	Ado24193 HIV epito
45	37	40.7	16	8	ADP02878	Adp02878 HIV gp120

ALIGNMENTS

RESULT 1
AAB92360
ID AAB92360 standard; peptide; 16 AA.
XX
AC AAB92360;
XX
DT 22-JUN-2001 (first entry)
XX
DE Miscellaneous peptide SEQ ID NO:1536.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 707; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic

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CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 91;  DB 4;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16


RESULT 2
ABP58217
ID   ABP58217 standard; peptide; 16 AA.
XX
AC   ABP58217;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Immunostimulant C3d peptide.
XX
KW   Immunostimulant; C3d; human; fusion protein; tumour; vaccine; adjuvant.
XX
OS   Homo sapiens.
XX
PN   WO200297041-A2.
XX
PD   05-DEC-2002.
XX
PF   29-MAY-2002; 2002WO-US016651.
XX
PR   29-MAY-2001; 2001US-00865281.
XX
PA   (IMMP-) IMMPHERON INC.
PA   (INNE-) INNEXUS CORP.
XX
PI   Kohler H,  Morgan C;
XX
DR   WPI; 2003-140458/13.
XX
PT   Novel fusion protein for use as molecular adjuvant, has an antibody and a
PT   peptide with immunostimulatory, membrane transport or homophilic
PT   activities, connected to the antibody by peptide bonds.
XX
PS   Example 1; Page 14; 39pp; English.
XX
CC   The present invention provides a fusion protein made up of an antibody
CC   and a peptide having e.g. immunostimulant, membrane transport or
CC   homophilic activity. The peptide is located at a site in the antibody
CC   such that it does not compromise the antigen recognition of the antibody.
CC   In order to enhance its activity, the peptide may be flanked by loop-
CC   forming or conformation-conferring sequences. The present sequence is an
CC   example of a suitable imunostimulatory peptide for use as a fusion
CC   protein component. The peptide is derived from human C3d amino acids 1217
CC   -1232. In examples from the invention, the C3d peptide was affinity cross
CC   -linked to tumour anti-idiotype and tumour idiotype vaccine antibodies,
CC   significantly enhancing the immune response to the tumour and protecting
CC   against tumour challenge. The vaccination protocol did not include any
CC   adjuvant, such as Freund's adjuvant or keyhole limpet haemocyanin
CC   conjugation, both of which are not permissible by the FDA for human use
XX
SQ   Sequence 16 AA;

  Query Match             100.0%;  Score 91;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16


RESULT 3
ADS17594
ID   ADS17594 standard; peptide; 16 AA.
XX
AC   ADS17594;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Peptide derived from the C3d peptide and affinity linked to 3H1 antibody.
XX
KW   immunostimulatory; membrane transport; homophilic; signaling protein;
KW   caspase; kinase; phosphatase; viral protein; tumour antigen;
KW   nuclear protein; nucleolar protein; DNA synthesis; cytoskeletal protein;
KW   cell proliferation; cytostasis; membrane transporter peptide;
KW   Kaposi fibroblast factor; TAT peptide; HIV-1; antennapedia homeodomain;
KW   herpes virus protein VP22; transportan peptide; Alzheimer's disease;
KW   Huntington's disease; Parkinson's disease; C3d; 3H1; monoclonal antibody;
KW   anti-idiotypic antibody; carcino-embryonic antigen; CEA;
KW   anti-idiotype vaccine; antibody.
XX
OS   Synthetic.
XX
PN   WO2004078146-A2.
XX
PD   16-SEP-2004.
XX
PF   05-MAR-2004; 2004WO-US006911.
XX
PR   05-MAR-2003; 2003US-0451980P.
XX
PA   (INNE-) INNEXUS BIOTECHNOLOGY INC.
PA   (IMMP-) IMMPHERON INC.
XX
PI   Kohler H,  Muller S,  Brown TL,  Zhao Y,  Morgan AC;
XX
DR   WPI; 2004-653567/63.
XX
PT   New compound for regulating normal or infected cell function comprising
PT   an antibody conjugated to a membrane transporter peptide, useful in
PT   preparing a composition for treating or preventing human diseases, e.g.
PT   Alzheimer's disease.
XX
PS   Example 1; SEQ ID NO 1; 50pp; English.
XX
CC   The specification describes a fusion protein for regulating normal or
CC   infected cell function, comprising an antibody conjugated to a peptide
CC   having immunostimulatory, membrane transport, and homophilic activities.
CC   The antibody is immunospecific for a signaling protein internal cell
CC   consisting of caspases, kinases or phosphatases, an immature viral
CC   protein, a cell-surface or intracellular tumour antigen, a nuclear or
CC   nucleolar protein participating in regulation of DNA synthesis and gene
CC   expression, or a cytoskeletal protein participating in cell proliferation
CC   or cytostasis. The peptide portion of the fusion protein is preferably a
CC   membrane transporter peptide that is endogenous to Kaposi fibroblast
CC   factor, TAT peptides of HIV-1, antennapedia homeodomain-derived peptide,
CC   herpes virus protein VP22, or transportan peptide. Fusion protein of the
CC   invention are useful for preparing a composition for treating or
CC   preventing human diseases, e.g., Alzheimer's disease, Huntington's
CC   disease or Parkinson's disease. The present sequence represents a peptide
CC   derived from the C3d region 1217-1232, which was affinity cross-linked
CC   with 3H1 monoclonal antibody to produce fusion proteins of the invention.
CC   3H1 is a murine anti-idiotypic antibody which mimics the carcino-
CC   embryonic antigen (CEA), and induces anti-CEA antibodies. The resulting
CC   Cd3-3H1 fusion protein was used to enhance an anti-idiotype vaccine.
XX
```

SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
||||||||||||||||
Db 1 KNRWEDPGKQLYNVEA 16

RESULT 4
ADV24825
ID ADV24825 standard; peptide; 16 AA.
XX
AC ADV24825;
XX
DT 24-FEB-2005 (first entry)
XX
DE CR2-binding complement C3d peptide, SEQ ID NO:2.
XX
KW Multivalent ligand; cell signaling; diagnostic; decontamination;
KW autoimmune disease; immune disorder; cancer; neoplasm; cancer metastasis;
KW immunosuppressive; immunomodulator; cytostatic; complement C3d.
XX
OS Unidentified.
XX
PN US2004248801-A1.
XX
PD 09-DEC-2004.
XX
PF 22-MAR-2004; 2004US-00806056.
XX
PR 21-MAR-2000; 2000US-0191014P.
PR 21-MAR-2001; 2001US-00815296.
PR 21-MAR-2003; 2003US-0456778P.
XX
PA (KIES/) KIESSLING L L.
PA (GRIF/) GRIFFITH B R.
PA (GEST/) GESTWICKI J E.
PA (STRO/) STRONG L.
XX
PI Kiessling LL, Griffith BR, Gestwicki JE, Strong L;
XX
DR WPI; 2005-046763/05.
XX
PT Novel multivalent ligand, useful for inducing biological response,
PT enhancing aggregation of biological particles and enhancing induction of
PT cellular response.
XX
PS Example 3; SEQ ID NO 2; 76pp; English.
XX
CC The invention relates to a multivalent ligand comprising a plurality of
CC signal recognition elements (SRE), binding recognition elements (BRE) and
CC functional elements (FE), and which is bonded to a polymeric scaffold.
CC The SREs are involved, either directly or indirectly, in biological
CC signaling processes, while the BREs facilitate the binding associated
CC with the process. Examples of SREs used in the multivalent ligand include
CC epitopes (especially one characteristic of a cancer cell), antigens,
CC antibodies or fragments thereof, cell surface receptors, polysaccharides,
CC nucleic acids or small drug-like compounds, and suitable BREs include
CC polysaccharides or metal-chelating groups which are optionally bound to
CC metals. The FE may be a detectable label, a reporter group or an enzyme.
CC The invention also relates to use of multivalent ligands in a method for
CC inducing a biological response in a biological system such as a cell or
CC organism which comprises one or more receptors recognized by an SRE; a
CC method of enhancing aggregation of biological particles such as cells or
CC viruses using a multivalent ligand complex which comprises several
CC recognition elements which each induce aggregation of one or more of the
CC biological particles; a method for inducing a cellular response or for
CC enhancing cellular response induction using a multivalent ligand; a
CC method of generating an assembly of biological macromolecules or
CC particles by providing a multivalent ligand comprising a molecular
CC scaffold to which several biological macromolecules or particles are
CC attached via BREs, wherein the number, density and spacing of the BREs is
CC controlled; and a library of multivalent ligands of the invention, in
CC which the members of the libraries vary in the type, number and/or
CC relative positioning of recognition elements, the combinations of BREs
CC and SREs present, the presence and/or positioning of spacers, the number
CC of repeating units or monomers, and the presence, type or number of FEs.
CC The invention also discloses pharmaceutical compositions comprising
CC multivalent ligands of the invention. The multivalent ligands are useful
CC for modulating immune system cell responses to epitopes, thereby
CC inhibiting or attenuating autoimmune disorders, and are also useful for
CC treating undesired cell proliferation (cancer) and undesired cell
CC migration (metastasis). They can be used in diagnostic applications for
CC the detection of biological molecules or particles in biological systems,
CC and are useful for preventing or inhibiting biofouling or removing
CC undesired cells in a selected environment. The present sequence
CC represents a complement C3d peptide able to bind complement receptor CR2
CC which may be used as a signal in a multivalent ligand for inducing an
CC enhanced immune response.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 91; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
||||||||||||||||
Db 1 KNRWEDPGKQLYNVEA 16

RESULT 5
AAW32826
ID AAW32826 standard; peptide; 16 AA.
XX
AC AAW32826;
XX
DT 17-OCT-2003 (revised)
DT 14-JAN-1998 (first entry)
XX
DE HIV-1 CDC4 envelope glycoprotein 120 T cell epitope T1.
XX
KW Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;
KW recognition; B lymphocyte; type specific; antibody; vaccine; protection;
KW immune response; infection; neutralisation; epitope.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9714436-A1.
XX
PD 24-APR-1997.
XX
PF 18-OCT-1996; 96WO-US016911.
XX
PR 20-OCT-1995; 95US-00546515.
PR 09-FEB-1996; 96US-00599266.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Palker TJ;
XX
DR WPI; 1997-244862/22.
XX
PT Synthetic human immunodeficiency virus vaccine - comprising hydrophilic
PT peptide corresponding to at least 1 antigenic determinant of envelope
PT glyco:protein recognised by B lymphocytes.
XX
PS Disclosure; Page 23; 104pp; English.
XX
CC An essentially pure hydrophilic peptide, comprising at least 1 antigenic
CC determinant of human immunodeficiency virus (HIV) envelope (env)
CC glycoprotein (gp) recognised by B lymphocytes, when covalently linked to
CC a carrier molecule, i.e. the present sequence, induces the production of

```
CC   high titres of protective, type specific anti-HIV antibodies (Ab) in a
CC   mammal. The peptide can be used in vaccines for producing a protective
CC   immune response to HIV infection, while a HIV neutralising Ab can be
CC   induced in a primate by administering a composition comprising HIV env
CC   peptides that disrupt gp120/gp41 interactions. (Updated on 17-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 16 AA;

  Query Match             41.8%;  Score 38;  DB 2;  Length 16;
  Best Local Similarity   54.5%;  Pred. No. 96;
  Matches    6;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              |||:  || :|
Db          5 NRWQVVGKAMY 15


RESULT 6
AAP82479
ID   AAP82479 standard; protein; 16 AA.
XX
AC   AAP82479;
XX
DT   25-MAR-2003  (revised)
DT   12-NOV-1990  (first entry)
XX
DE   Peptide component of AIDS vaccine.
XX
KW   AIDS vaccine; T-cells.
XX
OS   Synthetic.
XX
PN   EP273716-A.
XX
PD   06-JUL-1988.
XX
PF   23-DEC-1987;   87EP-00311391.
XX
PR   30-DEC-1986;   86US-00947935.
PR   12-FEB-1987;   87US-00014430.
XX
PA   (USDC ) US SEC OF COMMERCE.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
PI   Delisi C,  Margalit H,  Cornette JL,  Ouyang CS;
XX
DR   WPI; 1988-184640/27.
XX
PT   Synthetic peptide(s) as vaccines for AIDS - selected from peptide regions
PT   which can fold as a maximally amphipathic helix recognised by I cells.
XX
PS   Claim 9; Page 10; 16pp; English.
XX
CC   This peptide is a component of an AIDS vaccine. It can fold as a
CC   maximally amphipathic helix and is recognised by T-cells immune to the
CC   AIDS virus envelope protein. See also AAP82462-78. (Updated on 25-MAR-
CC   2003 to correct PA field.)
XX
SQ   Sequence 16 AA;

  Query Match             40.7%;  Score 37;  DB 1;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 7
AAR24424
ID   AAR24424 standard; peptide; 16 AA.
XX
AC   AAR24424;
XX
DT   25-MAR-2003  (revised)
DT   21-NOV-1992  (first entry)
XX
DE   Sequence of T helper peptide of gp120 at amino acid residue numbers 105-
DE   117(T2).
XX
KW   Vaccine; AIDS; HIV-1; carrier peptide.
XX
OS   Homo sapiens.
XX
PN   WO9208491-A1.
XX
PD   29-MAY-1992.
XX
PF   19-NOV-1991;   91WO-US008653.
XX
PR   20-NOV-1990;   90US-00616247.
XX
PA   (TANO-) TANOX BIOSYSTEMS INC.
XX
PI   Chang TW,  Fung MSC;
XX
DR   WPI; 1992-199955/24.
XX
PT   Vaccines comprising anti-idiotype antibody conjugates - induce prodn. of
PT   neutralising antibodies against HIV-1 for immunisation against HIV
PT   infection and AIDS.
XX
PS   Claim 12; Page 26 and page 15; 29pp; English.
XX
CC   The invention includes epitope-directed immunization with a vaccine in
CC   which an anti-idiotype antibody is conjugated to a carrier, which can be
CC   either a protein or its derived T helper peptide. The carrier is one
CC   against which the vaccine recipient has previously immunized or otherwise
CC   previously exposed, or which enhances the immune response against the
CC   anti-idiotype antibody. One exemplary anti-idiotype antibody which
CC   induces antibodies against the PND is AB19-4. Where the anti-idiotype
CC   induces Ab3 against HIV-1, the carrier preferably is HBsAg or HIV-1 p24,
CC   or a peptide of either HBsAg or HIV-1 p24 including a T helper
CC   determinant. "PND" = the principal neutralizing determinant ("PND") of
CC   gp120. A T-helper peptide with the sequence in AAR24423, or immunological
CC   equivalents of this sequence is suitable for conjugation with AB19-4 or
CC   other anti-idiotypes which induce Ab3 against HIV-1. (Updated on 25-MAR-
CC   2003 to correct PN field.)
XX
SQ   Sequence 16 AA;

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          6 NMWQEVGKAMY 16


RESULT 8
AAR85369
ID   AAR85369 standard; peptide; 16 AA.
XX
AC   AAR85369;
XX
DT   16-OCT-2003  (revised)
DT   12-JUN-1996  (first entry)
XX
DE   HTLV-IIIB gp120 envelope T cell eptope T1.
XX
KW   Human immunodeficiency virus; HIV; HTLV-IIIB; envelope; glycoprotein;
KW   hydrophilic; immunisation; antibody production; fusion peptide; SP-10;
KW   conjugate; carrier.
```

XX
OS Human immunodeficiency virus 1.
XX
PN WO9529700-A1.
XX
PD 09-NOV-1995.
XX
PF 28-APR-1995; 95WO-US005465.
XX
PR 29-APR-1994; 94US-00235305.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Palker TJ;
XX
DR WPI; 1995-392926/50.
XX
PT New peptide(s) corresponding to HIV sequences - used for inducing
PT protective immunity to HIV and in the treatment of e.g. auto-immune
PT disease, infectious disease or tumours.
XX
PS Claim 6; Page 16; 128pp; English.
XX
CC AAR85369 and AAR85370 are HTLV-IIIB gp120 envelope T cell epitopes T1 and
CC T2. The two peptides corresp. to amino acids 428-443 and 112-124 of the
CC HIV isolate, HTLV-IIIB gp120 envelope protein. The peptides can be
CC conjugated to SP-10 and "SP-10-like" regions of other HIV isolates.
CC Conjugates produced are capable of inducing the production of high titres
CC of protective, type-specific, anti-HIV antibodies. Helper T cells and
CC cytotoxic T cells are also activated by the peptide immunogens. (Updated
CC on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 16 AA;

Query Match 40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12
| |:: || :|
Db 5 NMWQEVGKAMY 15

RESULT 9
AAW07391
ID AAW07391 standard; peptide; 16 AA.
XX
AC AAW07391;
XX
DT 16-OCT-2003 (revised)
DT 24-FEB-1997 (first entry)
XX
DE HIV-1 CD4 binding site.
XX
KW HIV-1; gp120; V3 loop; common consensus PND domain; envelop; CD4;
KW binding site; stem-loop; lysine branched peptide; AIDS.
XX
OS Human immunodeficiency virus 1.
XX
PN JP08231423-A.
XX
PD 10-SEP-1996.
XX
PF 27-FEB-1995; 95JP-00038835.
XX
PR 27-FEB-1995; 95JP-00038835.
XX
PA (TERU) TERUMO CORP.
PA (OKUD/) OKUDA K.
XX
DR WPI; 1996-461278/46.
XX
PT Novel AIDS vaccine - comprises branched lysine peptide fragments derived
PT from HIV env protein.
XX
PS Example 1; Page 5; 8pp; Japanese.
XX
CC This is the CD4 binding site sequence from HIV-1. Part of the peptide
CC (from residues 4-16) was fused to part of the HIV-1 gp120 V3 loop common
CC consensus PND sequence (AAW07390) to form a stem-loop construct
CC (AAW07395). This construct was used with the V3 loop sequences from HIV-
CC 12 strains IIIB (AAW07392), Thai B (AAW07393) or HGP-30 (AAW07394) to
CC generate a lysine branched peptide which is useful for the prevention and
CC treatment of AIDS. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 16 AA;

Query Match 40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12
| |:: || :|
Db 5 NMWQEVGKAMY 15

RESULT 10
AAW10345
ID AAW10345 standard; peptide; 16 AA.
XX
AC AAW10345;
XX
DT 15-OCT-1997 (first entry)
XX
DE HIV epitope env T1 amino acid residues 428-443 of gp120.
XX
KW Human immunodeficiency virus type-1; HIV-1; T cell response; detection;
KW peripheral blood mononuclear cell; PBMC.
XX
OS Synthetic.
XX
PN WO9641189-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010108.
XX
PR 07-JUN-1995; 95US-00488435.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Shearer GM, Berzofsky JA, Clerici M;
XX
DR WPI; 1997-108658/10.
XX
PT Diagnosis of exposure to infectious agents, partic. HIV - by detecting
PT activation of peripheral blood mononuclear cells from patient by epitope
PT of infectious agent.
XX
PS Claim 15; Page 62; 82pp; English.
XX
CC The present sequence represents a synthetic HIV-1 gp120 peptide env T1
CC for use in a method for diagnosing exposure of a patient to human
CC immunodeficiency virus (HIV). The method involves: (a) obtaining
CC peripheral blood mononuclear cells (PBMC) from a patient; (b) incubating
CC the PBMC with at least 1 synthetic peptide representing an epitope(s) of
CC the infectious agent (e.g. the present sequence); and (c) determining the
CC activation of the PBMC as a result of the incubation in step (b). The
CC method can provide for the early detection of exposure to infectious
CC organisms, specifically HIV in this case. The method can be used to
CC assess exposure to HIV without concomitant infection. It also provides an
CC earlier identification of HIV exposure, than is provided by
CC seroconversion
XX
SQ Sequence 16 AA;

```
  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 11
AAW16512
ID   AAW16512 standard; peptide; 16 AA.
XX
AC   AAW16512;
XX
DT   14-JAN-1998  (first entry)
XX
DE   HTLV-IIIB envelope glycoprotein 120 T cell epitope T1.
XX
KW   Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;
KW   recognition; B lymphocyte; type specific; antibody; vaccine; protection;
KW   immune response; infection; neutralisation; epitope.
XX
OS   Human lymphotropic virus.
XX
PN   WO9714436-A1.
XX
PD   24-APR-1997.
XX
PF   18-OCT-1996;   96WO-US016911.
XX
PR   20-OCT-1995;   95US-00546515.
PR   09-FEB-1996;   96US-00599266.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Haynes BF,  Palker TJ;
XX
DR   WPI; 1997-244862/22.
XX
PT   Synthetic human immunodeficiency virus vaccine - comprising hydrophilic
PT   peptide corresponding to at least 1 antigenic determinant of envelope
PT   glyco:protein recognised by B lymphocytes.
XX
PS   Disclosure; Page 13; 104pp; English.
XX
CC   An essentially pure hydrophilic peptide, comprising at least 1 antigenic
CC   determinant of human immunodeficiency virus (HIV) envelope (env)
CC   glycoprotein (gp) recognised by B lymphocytes, when covalently linked to
CC   a carrier molecule, i.e. the present sequence, induces the production of
CC   high titres of protective, type specific anti-HIV antibodies (Ab) in a
CC   mammal. The peptide can be used in vaccines for producing a protective
CC   immune response to HIV infection, while a HIV neutralising Ab can be
CC   induced in a primate by administering a composition comprising HIV env
CC   peptides that disrupt gp120/gp41 interactions
XX
SQ   Sequence 16 AA;

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 12
AAW32824
ID   AAW32824 standard; peptide; 16 AA.
XX
AC   AAW32824;
XX
DT   17-OCT-2003  (revised)
DT   14-JAN-1998  (first entry)
XX
DE   HIV-1 SC envelope glycoprotein 120 T cell epitope T1.
XX
KW   Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;
KW   recognition; B lymphocyte; type specific; antibody; vaccine; protection;
KW   immune response; infection; neutralisation; epitope.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO9714436-A1.
XX
PD   24-APR-1997.
XX
PF   18-OCT-1996;   96WO-US016911.
XX
PR   20-OCT-1995;   95US-00546515.
PR   09-FEB-1996;   96US-00599266.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Haynes BF,  Palker TJ;
XX
DR   WPI; 1997-244862/22.
XX
PT   Synthetic human immunodeficiency virus vaccine - comprising hydrophilic
PT   peptide corresponding to at least 1 antigenic determinant of envelope
PT   glyco:protein recognised by B lymphocytes.
XX
PS   Disclosure; Page 23; 104pp; English.
XX
CC   An essentially pure hydrophilic peptide, comprising at least 1 antigenic
CC   determinant of human immunodeficiency virus (HIV) envelope (env)
CC   glycoprotein (gp) recognised by B lymphocytes, when covalently linked to
CC   a carrier molecule, i.e. the present sequence, induces the production of
CC   high titres of protective, type specific anti-HIV antibodies (Ab) in a
CC   mammal. The peptide can be used in vaccines for producing a protective
CC   immune response to HIV infection, while a HIV neutralising Ab can be
CC   induced in a primate by administering a composition comprising HIV env
CC   peptides that disrupt gp120/gp41 interactions. (Updated on 17-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 16 AA;

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 13
AAW16535
ID   AAW16535 standard; peptide; 16 AA.
XX
AC   AAW16535;
XX
DT   17-OCT-2003  (revised)
DT   14-JAN-1998  (first entry)
XX
DE   HIV-1 BH10 envelope glycoprotein 120 T cell epitope T1.
XX
KW   Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;
KW   recognition; B lymphocyte; type specific; antibody; vaccine; protection;
KW   immune response; infection; neutralisation; epitope.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO9714436-A1.
XX
```

PD 24-APR-1997.
XX
PF 18-OCT-1996; 96WO-US016911.
XX
PR 20-OCT-1995; 95US-00546515.
PR 09-FEB-1996; 96US-00599266.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Palker TJ;
XX
DR WPI; 1997-244862/22.
XX
PT Synthetic human immunodeficiency virus vaccine - comprising hydrophilic
PT peptide corresponding to at least 1 antigenic determinant of envelope
PT glyco:protein recognised by B lymphocytes.
XX
PS Disclosure; Page 23; 104pp; English.
XX
CC An essentially pure hydrophilic peptide, comprising at least 1 antigenic
CC determinant of human immunodeficiency virus (HIV) envelope (env)
CC glycoprotein (gp) recognised by B lymphocytes, when covalently linked to
CC a carrier molecule, i.e. the present sequence, induces the production of
CC high titres of protective, type specific anti-HIV antibodies (Ab) in a
CC mammal. The peptide can be used in vaccines for producing a protective
CC immune response to HIV infection, while a HIV neutralising Ab can be
CC induced in a primate by administering a composition comprising HIV env
CC peptides that disrupt gp120/gp41 interactions. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 16 AA;

Query Match 40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12
| |:: || :|
Db 5 NMWQEVGKAMY 15

RESULT 14
AAW32825
ID AAW32825 standard; peptide; 16 AA.
XX
AC AAW32825;
XX
DT 17-OCT-2003 (revised)
DT 14-JAN-1998 (first entry)
XX
DE HIV-1 SF2 envelope glycoprotein 120 T cell epitope T1.
XX
KW Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;
KW recognition; B lymphocyte; type specific; antibody; vaccine; protection;
KW immune response; infection; neutralisation; epitope.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9714436-A1.
XX
PD 24-APR-1997.
XX
PF 18-OCT-1996; 96WO-US016911.
XX
PR 20-OCT-1995; 95US-00546515.
PR 09-FEB-1996; 96US-00599266.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Palker TJ;
XX
DR WPI; 1997-244862/22.
XX
PT Synthetic human immunodeficiency virus vaccine - comprising hydrophilic
PT peptide corresponding to at least 1 antigenic determinant of envelope
PT glyco:protein recognised by B lymphocytes.
XX
PS Disclosure; Page 23; 104pp; English.
XX
CC An essentially pure hydrophilic peptide, comprising at least 1 antigenic
CC determinant of human immunodeficiency virus (HIV) envelope (env)
CC glycoprotein (gp) recognised by B lymphocytes, when covalently linked to
CC a carrier molecule, i.e. the present sequence, induces the production of
CC high titres of protective, type specific anti-HIV antibodies (Ab) in a
CC mammal. The peptide can be used in vaccines for producing a protective
CC immune response to HIV infection, while a HIV neutralising Ab can be
CC induced in a primate by administering a composition comprising HIV env
CC peptides that disrupt gp120/gp41 interactions. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 16 AA;

Query Match 40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12
| |:: || :|
Db 5 NMWQEVGKAMY 15

RESULT 15
AAW32822
ID AAW32822 standard; peptide; 16 AA.
XX
AC AAW32822;
XX
DT 17-OCT-2003 (revised)
DT 14-JAN-1998 (first entry)
XX
DE HIV-1 BRU envelope glycoprotein 120 T cell epitope T1.
XX
KW Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;
KW recognition; B lymphocyte; type specific; antibody; vaccine; protection;
KW immune response; infection; neutralisation; epitope.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9714436-A1.
XX
PD 24-APR-1997.
XX
PF 18-OCT-1996; 96WO-US016911.
XX
PR 20-OCT-1995; 95US-00546515.
PR 09-FEB-1996; 96US-00599266.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Palker TJ;
XX
DR WPI; 1997-244862/22.
XX
PT Synthetic human immunodeficiency virus vaccine - comprising hydrophilic
PT peptide corresponding to at least 1 antigenic determinant of envelope
PT glyco:protein recognised by B lymphocytes.
XX
PS Disclosure; Page 23; 104pp; English.
XX
CC An essentially pure hydrophilic peptide, comprising at least 1 antigenic
CC determinant of human immunodeficiency virus (HIV) envelope (env)
CC glycoprotein (gp) recognised by B lymphocytes, when covalently linked to
CC a carrier molecule, i.e. the present sequence, induces the production of
CC high titres of protective, type specific anti-HIV antibodies (Ab) in a
CC mammal. The peptide can be used in vaccines for producing a protective
CC immune response to HIV infection, while a HIV neutralising Ab can be

CC induced in a primate by administering a composition comprising HIV env
CC peptides that disrupt gp120/gp41 interactions. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 16 AA;

Query Match 40.7%; Score 37; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15
```

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GenCore version 5.1.8

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Run on: May 15, 2006, 16:39:16 ; Search time 45 Seconds
(without alignments)
29.396 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 7712

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	100.0	16	2	US-09-070-907-1	Sequence 1, Appli
2	91	100.0	16	2	US-09-623-548A-1536	Sequence 1536, Ap
3	91	100.0	16	2	US-09-657-276-1536	Sequence 1536, Ap
4	37	40.7	16	1	US-08-213-124-5	Sequence 5, Appli
5	37	40.7	16	1	US-08-488-252-35	Sequence 35, Appl
6	37	40.7	16	1	US-07-847-311A-15	Sequence 15, Appl
7	37	40.7	16	2	US-09-046-373-1	Sequence 1, Appli
8	37	40.7	16	2	US-09-009-953-230	Sequence 230, App
9	37	40.7	16	2	US-09-340-798A-40	Sequence 40, Appl
10	37	40.7	16	2	US-09-311-784A-308	Sequence 308, App
11	37	40.7	16	2	US-09-724-961-51	Sequence 51, Appl
12	37	40.7	16	2	US-09-580-018-51	Sequence 51, Appl
13	37	40.7	16	2	US-09-724-551-51	Sequence 51, Appl
14	37	40.7	16	2	US-09-862-849-1	Sequence 1, Appli
15	37	40.7	16	2	US-10-114-716A-1	Sequence 1, Appli
16	37	40.7	16	2	US-09-724-953-9	Sequence 9, Appli
17	37	40.7	16	2	US-09-724-567-9	Sequence 9, Appli
18	37	40.7	16	2	US-09-724-940-51	Sequence 51, Appl
19	37	40.7	16	2	US-09-979-952-9	Sequence 9, Appli
20	37	40.7	16	2	US-09-585-817-9	Sequence 9, Appli
21	29	31.9	16	1	US-08-257-528B-22	Sequence 22, Appl
22	29	31.9	16	1	US-08-460-602A-22	Sequence 22, Appl
23	29	31.9	16	1	US-08-463-966A-22	Sequence 22, Appl
24	29	31.9	16	1	US-08-465-217A-22	Sequence 22, Appl
25	29	31.9	16	1	US-08-464-329A-22	Sequence 22, Appl
26	29	31.9	16	1	US-08-462-507A-22	Sequence 22, Appl
27	29	31.9	16	1	US-08-467-881A-22	Sequence 22, Appl
28	29	31.9	16	1	US-08-312-202B-4	Sequence 4, Appli
29	29	31.9	16	2	US-09-079-347-4	Sequence 4, Appli
30	29	31.9	16	2	US-09-075-725-4	Sequence 4, Appli
31	29	31.9	16	2	US-08-809-646-4	Sequence 4, Appli
32	29	31.9	16	4	PCT-US95-12433-4	Sequence 4, Appli
33	26.5	29.1	16	2	US-09-996-288-41	Sequence 41, Appl
34	26.5	29.1	16	2	US-09-996-288-114	Sequence 114, App
35	26.5	29.1	16	2	US-09-996-265-41	Sequence 41, Appl
36	26.5	29.1	16	2	US-09-996-265-114	Sequence 114, App
37	26	28.6	16	1	US-08-471-780C-69	Sequence 69, Appl
38	26	28.6	16	1	US-08-467-282B-69	Sequence 69, Appl
39	26	28.6	16	1	US-08-179-557-37	Sequence 37, Appl
40	26	28.6	16	1	US-08-471-282A-69	Sequence 69, Appl
41	26	28.6	16	1	US-08-466-710C-69	Sequence 69, Appl
42	26	28.6	16	2	US-08-468-739C-69	Sequence 69, Appl
43	26	28.6	16	2	US-09-141-882A-8	Sequence 8, Appli
44	26	28.6	16	2	US-08-981-601-12	Sequence 12, Appl
45	26	28.6	16	2	US-09-452-142-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-09-070-907-1
; Sequence 1, Application US/09070907
; Patent No. 6238667
; GENERAL INFORMATION:
;  APPLICANT: Kohler, Heinz
;  TITLE OF INVENTION: METHOD OF AFFINITY CROSS-LINKING BIOLOGICALLY ACTIVE
;  TITLE OF INVENTION: IMMUNOGENIC PEPTIDES TO ANTIBODIES.
;  FILE REFERENCE: 35629
;  CURRENT APPLICATION NUMBER: US/09/070,907
;  CURRENT FILING DATE: 1998-05-04
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: AMINO ACID
;   OTHER INFORMATION: SEQUENCE DERIVED FROM Cd3 peptide
US-09-070-907-1

  Query Match             100.0%;  Score 91;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-09;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16


RESULT 2
US-09-623-548A-1536
; Sequence 1536, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
;  APPLICANT: Conjuchem, Inc.
;  APPLICANT:  Bridon, Dominique
;  APPLICANT:  Ezrin, Alan
;  APPLICANT:  Milner, Peter
;  APPLICANT:  Holmes, Darren
;  APPLICANT:  Thibaudeau, Karen
;  TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;  TITLE OF INVENTION:  PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;  TITLE OF INVENTION:  COMPONENTS
;  FILE REFERENCE: 2110
;  CURRENT APPLICATION NUMBER: US/09/623,548A
;  CURRENT FILING DATE:  2000-09-05
;  PRIOR APPLICATION NUMBER: 60/134,406
;  PRIOR FILING DATE: 1999-05-17
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;  PRIOR APPLICATION NUMBER: 60/153,406
;  PRIOR FILING DATE: 1999-09-10
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-18
;  NUMBER OF SEQ ID NOS: 1617
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1536
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-623-548A-1536

  Query Match             100.0%;  Score 91;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-09;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16


RESULT 3
US-09-657-276-1536
; Sequence 1536, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
;  APPLICANT:  Conjuchem, Inc.
;  APPLICANT:  Bridon, Dominique
;  APPLICANT:  Ezrin, Alan
;  APPLICANT:  Milner, Peter
;  APPLICANT:  Holmes, Darren
;  APPLICANT:  Thibaudeau, Karen
;  TITLE OF INVENTION:  PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;  TITLE OF INVENTION:  PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;  TITLE OF INVENTION:  COMPONENTS
;  FILE REFERENCE:  2110
;  CURRENT APPLICATION NUMBER: US/09/657,276
;  CURRENT FILING DATE:  2000-09-07
;  PRIOR APPLICATION NUMBER:  60/134,406
;  PRIOR FILING DATE:  1999-05-17
;  PRIOR APPLICATION NUMBER:  60/153,406
;  PRIOR FILING DATE:  1999-09-10
;  PRIOR APPLICATION NUMBER:  60/159,783
;  PRIOR FILING DATE:  1999-10-18
;  NUMBER OF SEQ ID NOS:  1617
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1536
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-09-657-276-1536

  Query Match             100.0%;  Score 91;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-09;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16


RESULT 4
US-08-213-124-5
; Sequence 5, Application US/08213124
; Patent No. 5693325
;  GENERAL INFORMATION:
;    APPLICANT:  Kahn, Michael
;    TITLE OF INVENTION:  PEPTIDE VACCINES AND METHODS RELATING
;    TITLE OF INVENTION:  THERETO
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/213,124
;      FILING DATE:  15-MAR-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hermanns, Karl R.
;      REGISTRATION NUMBER:  33,507
;      REFERENCE/DOCKET NUMBER:  670063.411
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;      TELEX:  3723836 SEEDANDBERRY
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-213-124-5

  Query Match             40.7%;  Score 37;  DB 1;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 5
US-08-488-252-35
; Sequence 35, Application US/08488252
; Patent No. 5763160
;  GENERAL INFORMATION:
;    APPLICANT:  Chang Yi Wang
;    TITLE OF INVENTION:  SYNTHETIC PEPTIDES AND PROCESS
;    TITLE OF INVENTION:  OF USING SAME FOR THE DETECTION OF ANTIBODIES TO
;    TITLE OF INVENTION:  HUMAN IMMUNODEFICIENCY VIRUS (HIV) GP120 ENVELOPE
;    TITLE OF INVENTION:  PROTEIN, DIAGNOSIS OF AIDS AND PRE-AIDS CONDITIONS
;    TITLE OF INVENTION:  AND AS VACCINES
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVE.
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,252
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
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;       APPLICATION NUMBER:  08\326,676
;       FILING DATE:  07-Jun-1995
;       APPLICATION NUMBER:  07\726,605
;       FILING DATE:  09-July-1991
;       APPLICATION NUMBER:  07\663,262
;       FILING DATE:  01-Mar-1991
;       APPLICATION NUMBER:  07\155,321
;       FILING DATE:  12-Feb-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Maria C. H. Lin
;       REGISTRATION NUMBER:  29,323
;       REFERENCE/DOCKET NUMBER:  1151-4004 US4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-758-4800
;       TELEFAX:  (212) 751-6849
;       TELEX:  421792
;   INFORMATION FOR SEQ ID NO:  35:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 amino acids
;       TYPE:  Amino acids
;       STRANDEDNESS:
;       TOPOLOGY:  Unknown
US-08-488-252-35

  Query Match             40.7%;  Score 37;  DB 1;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 6
US-07-847-311A-15
; Sequence 15, Application US/07847311A
; Patent No. 5976541
;  GENERAL INFORMATION:
;     APPLICANT:  Berzofsky, Jay A.
;     APPLICANT:  Takeshita, Toshiyuki
;     APPLICANT:  Shirai, Mutsunori
;     APPLICANT:  Pendleton, C.D.
;     APPLICANT:  Koslowski, Steven
;     APPLICANT:  Margulies, David H.
;     TITLE OF INVENTION:  Potent Peptide for Stimulation of
;     TITLE OF INVENTION:  Cytotoxic T Lymphocytes Specific for the HIV-I Envelope
;     NUMBER OF SEQUENCES:  20
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Birch, Stewart, Kolash & Birch
;       STREET:  301 N. Washington
;       CITY:  Falls Church
;       STATE:  Virginia
;       COUNTRY:  USA
;       ZIP:  22046-0747
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/847,311A
;       FILING DATE:  06-MAR-1992
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Svensson, Leonard R.
;       REGISTRATION NUMBER:  30,330
;       REFERENCE/DOCKET NUMBER:  1173-392P
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  703-241-1300
;       TELEFAX:  703-241-2848
;   INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
;       ORGANISM:  Human Immunodeficiency Virus Type I
;     FEATURE:
;       NAME/KEY:  Peptide
;       LOCATION:  1..16
;       OTHER INFORMATION:  /label= peptide
;       OTHER INFORMATION:  /note= "peptide T1, T-cell helper determinant in
;       OTHER INFORMATION:  HIV-I envelope glycoprote..."
US-07-847-311A-15

  Query Match             40.7%;  Score 37;  DB 1;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 7
US-09-046-373-1
; Sequence 1, Application US/09046373
; Patent No. 6235714
; GENERAL INFORMATION:
;  APPLICANT: Sudhir Paul
;  APPLICANT: Larry J. Smith
;  APPLICANT: Gennady Gololobov
;  TITLE OF INVENTION: Methods for Identifying Inducers and
;  TITLE OF INVENTION: Inhibitors of Catalytic Antibodies, Compositions and Their
;  TITLE OF INVENTION: Use
;  FILE REFERENCE: UNMC 63123
;  CURRENT APPLICATION NUMBER: US/09/046,373
;  CURRENT FILING DATE: 1998-03-23
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Human Immunodeficiency Virus-1
US-09-046-373-1

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 8
US-09-009-953-230
; Sequence 230, Application US/09009953
; Patent No. 6413517
;   GENERAL INFORMATION:
;        APPLICANT: Sette, Alessandro
;        TITLE OF INVENTION: Identification of Broadly
;                            Reactive DR Restricted Epitopes
;        NUMBER OF SEQUENCES: 274
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
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;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/009,953
;             FILING DATE: 21-Jan-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 60/036,713
;             FILING DATE: 23-JAN-1997
;             APPLICATION NUMBER: US 60/037,432
;             FILING DATE: 07-FEB-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Weber, Ellen Lauver
;             REGISTRATION NUMBER: 32,762
;             REFERENCE/DOCKET NUMBER: 018623-011520US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-576-0200
;             TELEFAX: 415-576-0300
;             TELEX: <Unknown>
;    INFORMATION FOR SEQ ID NO: 230:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 230:
US-09-009-953-230

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          6 NMWQEVGKAMY 16


RESULT 9
US-09-340-798A-40
; Sequence 40, Application US/09340798A
; Patent No. 6534312
;   GENERAL INFORMATION:
;        APPLICANT: SHIVER, JOHN W.
;                   LIU, MARGARET A.
;                   PERRY, HELEN C.
;                   DAVIES, MARY-ELLEN M.
;                   FREED, DANIEL C.
;        TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES
;        NUMBER OF SEQUENCES: 53
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
;             STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
;             CITY: RAHWAY
;             STATE: NEW JERSEY
;             COUNTRY: US
;             ZIP: 07065-0907
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/340,798A
;             FILING DATE: 28-Jun-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/877,418
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: HAND, J. MARK
;             REGISTRATION NUMBER: 36,545
;             REFERENCE/DOCKET NUMBER: 19729Y
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 908-594-3905
;             TELEFAX: 908-594-4720
;    INFORMATION FOR SEQ ID NO: 40:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-340-798A-40

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 10
US-09-311-784A-308
; Sequence 308, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.01
;  CURRENT APPLICATION NUMBER: US/09/311,784A
;  CURRENT FILING DATE:  1999-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HIV1 ENV 566 (peptide F091.15)
US-09-311-784A-308

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          6 NMWQEVGKAMY 16


RESULT 11
US-09-724-961-51
; Sequence 51, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
;  APPLICANT: Schenk, Dale B.
;  APPLICANT:  Bard, Frederique
;  APPLICANT:  Vasquez, Nicki
;  APPLICANT:  Yednock, Ted
;  TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
;  FILE REFERENCE: 15270J-004750UC
;  CURRENT APPLICATION NUMBER: US/09/724,961
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;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: US 09/580,015
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/322,289
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: US 09/201,430
;  PRIOR FILING DATE: 1998-11-30
;  PRIOR APPLICATION NUMBER: WO PCT/US00/14810
;  PRIOR FILING DATE: 1998-11-30
;  PRIOR APPLICATION NUMBER: US 60/080,970
;  PRIOR FILING DATE: 1998-04-07
;  PRIOR APPLICATION NUMBER: US 60/067,740
;  PRIOR FILING DATE: 1997-12-02
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:HIV gp120 T1
;   OTHER INFORMATION: universal T-cell epitope
US-09-724-961-51

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 12
US-09-580-018-51
; Sequence 51, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
;  APPLICANT: Schenk, Dale B.
;  APPLICANT:  Bard, Frederique
;  APPLICANT:  Yednock, Ted
;  TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
;  FILE REFERENCE: 15270J-004760US
;  CURRENT APPLICATION NUMBER: US/09/580,018
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/322,289
;  PRIOR FILING DATE: 1999-05-28
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:HIV gp120 T1
;   OTHER INFORMATION: universal T-cell epitope
US-09-580-018-51

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 13
US-09-724-551-51
; Sequence 51, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
;  APPLICANT: Schenk, Dale B.
;  APPLICANT:  Bard, Frederique
;  APPLICANT:  Yednock, Ted
;  TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
;  FILE REFERENCE: 15270J-004760US
;  CURRENT APPLICATION NUMBER: US/09/724,551
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: US/09/580,018
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/322,289
;  PRIOR FILING DATE: 1999-05-28
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:HIV gp120 T1
;   OTHER INFORMATION: universal T-cell epitope
US-09-724-551-51

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 14
US-09-862-849-1
; Sequence 1, Application US/09862849
; Patent No. 6855528
; GENERAL INFORMATION:
;  APPLICANT: Sudhir Paul
;  APPLICANT:  Larry J. Smith
;  APPLICANT:  Gennady Gololobov
;  TITLE OF INVENTION: Methods for Identifying Inducers and Inhibitors of Proteolytic
;  TITLE OF INVENTION:  Antibodies, Compositions and Their Uses
;  FILE REFERENCE: UNMC 63123 DIV
;  CURRENT APPLICATION NUMBER: US/09/862,849
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: US 09/046,373
;  PRIOR FILING DATE: 1998-03-23
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Human Immunodeficiency Virus-1
US-09-862-849-1

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 15
US-10-114-716A-1
; Sequence 1, Application US/10114716A
; Patent No. 6855804
; GENERAL INFORMATION:
;  APPLICANT: Sudhir Paul
;  APPLICANT:  Yasuhiro Nishiyama
;  TITLE OF INVENTION: Covalently Reactive Transition State
;  TITLE OF INVENTION:  Analogs and Methods of Use Thereof
;  FILE REFERENCE: UTH001HB
;  CURRENT APPLICATION NUMBER: US/10/114,716A
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;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 09/862,849
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: 09/046,373
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 60/280,624
;  PRIOR FILING DATE: 2001-03-31
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Human Immunodeficiency Virus-1
US-10-114-716A-1

  Query Match             40.7%;  Score 37;  DB 2;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 11;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


Search completed: May 15, 2006, 16:40:32
Job time : 46 secs
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GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 15, 2006, 16:50:07 ; Search time 159 Seconds
(without alignments)
42.046 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 11256

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	100.0	16	3	US-09-865-281A-1	Sequence 1, Appli
2	91	100.0	16	5	US-10-795-081A-1	Sequence 1, Appli
3	91	100.0	16	6	US-11-066-697-1536	Sequence 1536, Ap
4	37	40.7	16	3	US-09-775-805-44	Sequence 44, Appl
5	37	40.7	16	3	US-09-775-805-67	Sequence 67, Appl
6	37	40.7	16	3	US-09-775-805-75	Sequence 75, Appl
7	37	40.7	16	3	US-09-775-805-89	Sequence 89, Appl
8	37	40.7	16	3	US-09-862-849-1	Sequence 1, Appli
9	37	40.7	16	3	US-09-894-018-199	Sequence 199, App
10	37	40.7	16	3	US-09-894-594-66	Sequence 66, Appl
11	37	40.7	16	4	US-10-103-395-230	Sequence 230, App
12	37	40.7	16	4	US-10-114-716A-1	Sequence 1, Appli
13	37	40.7	16	4	US-10-041-414-42	Sequence 42, Appl
14	37	40.7	16	4	US-10-371-525-308	Sequence 308, App
15	37	40.7	16	4	US-10-371-069-308	Sequence 308, App
16	37	40.7	16	4	US-10-371-645-308	Sequence 308, App
17	37	40.7	16	4	US-10-371-260-308	Sequence 308, App
18	37	40.7	16	4	US-10-369-121-40	Sequence 40, Appl
19	37	40.7	16	4	US-10-372-111-9	Sequence 9, Appli
20	37	40.7	16	4	US-10-699-517-11	Sequence 11, Appl
21	37	40.7	16	4	US-10-698-099-11	Sequence 11, Appl
22	37	40.7	16	4	US-10-753-339-44	Sequence 44, Appl
23	37	40.7	16	4	US-10-753-339-67	Sequence 67, Appl
24	37	40.7	16	4	US-10-753-339-75	Sequence 75, Appl
25	37	40.7	16	4	US-10-753-339-89	Sequence 89, Appl
26	37	40.7	16	4	US-10-771-174A-10	Sequence 10, Appl
27	37	40.7	16	5	US-10-889-999-51	Sequence 51, Appl
28	37	40.7	16	5	US-10-890-070-51	Sequence 51, Appl
29	37	40.7	16	5	US-10-474-960A-199	Sequence 199, App
30	37	40.7	16	5	US-10-890-000-51	Sequence 51, Appl
31	37	40.7	16	5	US-10-823-463-51	Sequence 51, Appl
32	37	40.7	16	5	US-10-915-214-11	Sequence 11, Appl
33	37	40.7	16	5	US-10-822-968-51	Sequence 51, Appl
34	37	40.7	16	5	US-10-777-792-51	Sequence 51, Appl
35	37	40.7	16	5	US-10-890-071-51	Sequence 51, Appl
36	37	40.7	16	5	US-10-930-548-1	Sequence 1, Appli
37	37	40.7	16	5	US-10-890-024-51	Sequence 51, Appl
38	37	40.7	16	5	US-10-928-926-51	Sequence 51, Appl
39	37	40.7	16	6	US-11-058-757-51	Sequence 51, Appl
40	37	40.7	16	6	US-11-058-728-1	Sequence 1, Appli
41	34	37.4	16	3	US-09-911-838-225	Sequence 225, App
42	32	35.2	16	4	US-10-289-228-65	Sequence 65, Appl
43	32	35.2	16	4	US-10-373-592-119	Sequence 119, App
44	32	35.2	16	4	US-10-431-596-65	Sequence 65, Appl
45	32	35.2	16	6	US-11-102-403-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-865-281A-1
; Sequence 1, Application US/09865281A
; Publication No. US20030103984A1
; GENERAL INFORMATION:
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: FUSION PROTEINS OF BIOLOGICALLY ACTIVE PEPTIDES AND ANTIBODIES
; FILE REFERENCE: 411.35629PC2
; CURRENT APPLICATION NUMBER: US/09/865,281A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/070,907
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(16)
; OTHER INFORMATION: Synthesized peptide with sequence derived from position 1217-123
US-09-865-281A-1

Query Match 100.0%; Score 91; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNRWEDPGKQLYNVEA 16
||||||||||||||||
Db 1 KNRWEDPGKQLYNVEA 16

RESULT 2
US-10-795-081A-1
; Sequence 1, Application US/10795081A
; Publication No. US20050033033A1
; GENERAL INFORMATION:
; APPLICANT: Kohler, Heinz
; TITLE OF INVENTION: TRANS-MEMBRANE-ANTIBODY INDUCED INHIBITION OF APOPTOSIS
; FILE REFERENCE: 411.35629AP3
; CURRENT APPLICATION NUMBER: US/10/795,081A
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 60/451,980
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 09/865,281
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/070,907
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 14

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;  SOFTWARE: Patentln version 3.0
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(16)
;   OTHER INFORMATION: Synthesized peptide with sequence derived from position 1217-1232
US-10-795-081A-1

  Query Match             100.0%;  Score 91;  DB 5;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16


RESULT 3
US-11-066-697-1536
; Sequence 1536, Application US/11066697
; Publication No. US20050187159A1
; GENERAL INFORMATION:
;  APPLICANT: Bridon, Dominique P.
;  APPLICANT:  Ezrin, Alan M.
;  APPLICANT:  Milner, Peter G.
;  APPLICANT:  Holmes, Darren L.
;  APPLICANT:  Thibaudeau, Karen
;  TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;  TITLE OF INVENTION:  PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;  TITLE OF INVENTION:  COMPONENTS
;  FILE REFERENCE: 500862002301
;  CURRENT APPLICATION NUMBER: US/11/066,697
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: 09/657,276
;  PRIOR FILING DATE: 2000-09-07
;  PRIOR APPLICATION NUMBER: 60/153,406
;  PRIOR FILING DATE: 1999-09-10
;  PRIOR APPLICATION NUMBER: 60/159,783
;  PRIOR FILING DATE: 1999-10-15
;  NUMBER OF SEQ ID NOS: 1617
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1536
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-066-697-1536

  Query Match             100.0%;  Score 91;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQLYNVEA 16
              ||||||||||||||||
Db          1 KNRWEDPGKQLYNVEA 16


RESULT 4
US-09-775-805-44
; Sequence 44, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
;  APPLICANT: DUKE UNIVERSITY
;  TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
;  FILE REFERENCE: 1579-548
;  CURRENT APPLICATION NUMBER: US/09/775,805
;  CURRENT FILING DATE:  2001-02-05
;  PRIOR APPLICATION NUMBER: 09/497,497
;  PRIOR FILING DATE: 2000-02-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Murine sp.
US-09-775-805-44

  Query Match             40.7%;  Score 37;  DB 3;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 5
US-09-775-805-67
; Sequence 67, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
;  APPLICANT: DUKE UNIVERSITY
;  TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
;  FILE REFERENCE: 1579-548
;  CURRENT APPLICATION NUMBER: US/09/775,805
;  CURRENT FILING DATE:  2001-02-05
;  PRIOR APPLICATION NUMBER: 09/497,497
;  PRIOR FILING DATE: 2000-02-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-775-805-67

  Query Match             40.7%;  Score 37;  DB 3;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 6
US-09-775-805-75
; Sequence 75, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
;  APPLICANT: DUKE UNIVERSITY
;  TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
;  FILE REFERENCE: 1579-548
;  CURRENT APPLICATION NUMBER: US/09/775,805
;  CURRENT FILING DATE:  2001-02-05
;  PRIOR APPLICATION NUMBER: 09/497,497
;  PRIOR FILING DATE: 2000-02-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV-1
;   OTHER INFORMATION: Th-dominant/subdominant CTL epitopes in MVA.
US-09-775-805-75

  Query Match             40.7%;  Score 37;  DB 3;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;
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```
Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 7
US-09-775-805-89
; Sequence 89, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
;  APPLICANT: DUKE UNIVERSITY
;  TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
;  FILE REFERENCE: 1579-548
;  CURRENT APPLICATION NUMBER: US/09/775,805
;  CURRENT FILING DATE:  2001-02-05
;  PRIOR APPLICATION NUMBER: 09/497,497
;  PRIOR FILING DATE: 2000-02-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HIV-1 Th-CTL
;   OTHER INFORMATION: A2 p17 epitope (A2 Variants) in MVA
US-09-775-805-89

  Query Match             40.7%;  Score 37;  DB 3;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 8
US-09-862-849-1
; Sequence 1, Application US/09862849
; Patent No. US20020013274A1
; GENERAL INFORMATION:
;  APPLICANT: Sudhir Paul
;  APPLICANT:  Larry J. Smith
;  APPLICANT:  Gennady Gololobov
;  TITLE OF INVENTION: Methods for Identifying Inducers and Inhibitors of Proteolytic
;  TITLE OF INVENTION:  Antibodies, Compositions and Their Uses
;  FILE REFERENCE: UNMC 63123 DIV
;  CURRENT APPLICATION NUMBER: US/09/862,849
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: US 09/046,373
;  PRIOR FILING DATE: 1998-03-23
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Human Immunodeficiency Virus-1
US-09-862-849-1

  Query Match             40.7%;  Score 37;  DB 3;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 9
US-09-894-018-199
; Sequence 199, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
;  APPLICANT: EPIMMUNE, Inc.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Chestnut, Robert
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Baker, Denisw
;  APPLICANT:  Newman, Mark
;  APPLICANT:  Brown, David
;  TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
;  TITLE OF INVENTION:  MINIGENES AND PEPTIDES THEREBY
;  FILE REFERENCE: 39963-20033.00
;  CURRENT APPLICATION NUMBER: US/09/894,018
;  CURRENT FILING DATE:  2001-06-27
;  PRIOR APPLICATION NUMBER: PCT/US00/35568
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: US 60/173,390
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: US 60/284,221
;  PRIOR FILING DATE: 2001-04-16
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 199
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Transgenic mouse
US-09-894-018-199

  Query Match             40.7%;  Score 37;  DB 3;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          6 NMWQEVGKAMY 16


RESULT 10
US-09-894-594-66
; Sequence 66, Application US/09894594
; Publication No. US20030017497A1
; GENERAL INFORMATION:
;  APPLICANT: Kieber-Emmons, Thomas
;  APPLICANT:  Weiner, David B.
;  APPLICANT:  Monzavi-Karbassi, Behjatolah
;  TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Enc
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: UPN-3984
;  CURRENT APPLICATION NUMBER: US/09/894,594
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: 09/601,558
;  PRIOR FILING DATE: 2000-11-07
;  PRIOR APPLICATION NUMBER: PCT/US99/02405
;  PRIOR FILING DATE: 1999-02-04
;  PRIOR APPLICATION NUMBER: 60/073,690
;  PRIOR FILING DATE: 1998-02-04
;  PRIOR APPLICATION NUMBER: 60/214,517
;  PRIOR FILING DATE: 2000-06-28
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Novel Sequence
US-09-894-594-66

  Query Match             40.7%;  Score 37;  DB 3;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 11
US-10-103-395-230
; Sequence 230, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
;  APPLICANT: EPIMMUNE, Inc.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
;  TITLE OF INVENTION:  RESTRICTED EPITOPES
;  FILE REFERENCE: 39963-20016.01
;  CURRENT APPLICATION NUMBER: US/10/103,395
;  CURRENT FILING DATE:  2003-01-03
;  PRIOR APPLICATION NUMBER: US 09/009,953
;  PRIOR FILING DATE: 1998-01-21
;  PRIOR APPLICATION NUMBER: PCT/US98/01373
;  PRIOR FILING DATE: 1998-01-23
;  PRIOR APPLICATION NUMBER: US 60/036,713
;  PRIOR FILING DATE: 1997-01-23
;  PRIOR APPLICATION NUMBER: US 60/037,432
;  PRIOR FILING DATE: 1997-02-07
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-103-395-230

  Query Match             40.7%;  Score 37;  DB 4;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          6 NMWQEVGKAMY 16


RESULT 12
US-10-114-716A-1
; Sequence 1, Application US/10114716A
; Publication No. US20030078203A1
; GENERAL INFORMATION:
;  APPLICANT: Sudhir Paul
;  APPLICANT:  Yasuhiro Nishiyama
;  TITLE OF INVENTION: Covalently Reactive Transition State
;  TITLE OF INVENTION:  Analogs and Methods of Use Thereof
;  FILE REFERENCE: UTH001HB
;  CURRENT APPLICATION NUMBER: US/10/114,716A
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 09/862,849
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: 09/046,373
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 60/280,624
;  PRIOR FILING DATE: 2001-03-31
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Human Immunodeficiency Virus-1
US-10-114-716A-1

  Query Match             40.7%;  Score 37;  DB 4;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 13
US-10-041-414-42
; Sequence 42, Application US/10041414
; Publication No. US20030087225A1
;   GENERAL INFORMATION:
;        APPLICANT: SHIVER, JOHN W.
;                   DAVIES, MARY ELLEN
;                   FREED, DANIEL C.
;                   LIU, MARGARET A.
;                   PERRY, HELEN C.
;        TITLE OF INVENTION: SYNTHETIC HIV ENV GENES
;        NUMBER OF SEQUENCES: 53
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
;             STREET: 126 E. LINCOLN AVE., - P.O. BOX 2000
;             CITY: RAHWAY
;             STATE: NEW JERSEY
;             COUNTRY: US
;             ZIP: 07065-0907
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/041,414
;             FILING DATE: 08-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/802,368
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: HAND, J. MARK
;             REGISTRATION NUMBER: 36,545
;             REFERENCE/DOCKET NUMBER: 19643
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 732-594-3905
;             TELEFAX: 732-594-4720
;   INFORMATION FOR SEQ ID NO: 42:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 16 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-041-414-42

  Query Match             40.7%;  Score 37;  DB 4;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 14
US-10-371-525-308
; Sequence 308, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
```

```
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.01
;  CURRENT APPLICATION NUMBER: US/10/371,525
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 09/311,784
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HIV1 ENV 566 (peptide F091.15)
US-10-371-525-308

  Query Match             40.7%;  Score 37;  DB 4;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          6 NMWQEVGKAMY 16


RESULT 15
US-10-371-069-308
; Sequence 308, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
;  APPLICANT: EPIMMUNE Inc.
;  APPLICANT:  Fikes, John D.
;  APPLICANT:  Hermanson, Gary G.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Ishioka, Glenn Y.
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert W.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Expression Vectors for Stimulating an
;  TITLE OF INVENTION:  Immune Response and Methods of Using the Same
;  FILE REFERENCE: 39963-20022.10
;  CURRENT APPLICATION NUMBER: US/10/371,069
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 09/078,904
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: US 60/085,751
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HIV1 ENV 566 (peptide F091.15)
US-10-371-069-308

  Query Match             40.7%;  Score 37;  DB 4;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 76;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          6 NMWQEVGKAMY 16


Search completed: May 15, 2006, 16:53:41
Job time : 160 secs
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GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 15, 2006, 16:51:11 ; Search time 27 Seconds
(without alignments)
27.822 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 2020

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep1:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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7: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep1:*
8: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
9: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep1:*
10: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
11: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep1:*
12: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	37	40.7	16	9	US-10-973-977-44	Sequence 44, Appl
2	37	40.7	16	9	US-10-973-977-67	Sequence 67, Appl
3	37	40.7	16	9	US-10-973-977-75	Sequence 75, Appl
4	37	40.7	16	9	US-10-973-977-89	Sequence 89, Appl
5	37	40.7	16	11	US-11-045-024-14479	Sequence 14479, A
6	37	40.7	16	11	US-11-115-425-88	Sequence 88, Appl
7	37	40.7	16	11	US-11-185-907-11	Sequence 11, Appl
8	32	35.2	16	11	US-11-056-950-226	Sequence 226, App
9	32	35.2	16	11	US-11-056-950-230	Sequence 230, App
10	32	35.2	16	11	US-11-056-950-234	Sequence 234, App
11	32	35.2	16	11	US-11-056-950-241	Sequence 241, App
12	30	33.0	16	11	US-11-056-950-54	Sequence 54, Appl
13	28	30.8	16	9	US-10-530-061-1652	Sequence 1652, Ap
14	27	29.7	16	11	US-11-056-950-185	Sequence 185, App
15	27	29.7	16	11	US-11-056-950-189	Sequence 189, App
16	27	29.7	16	11	US-11-056-950-193	Sequence 193, App
17	27	29.7	16	11	US-11-056-950-204	Sequence 204, App
18	26	28.6	16	11	US-11-056-950-208	Sequence 208, App
19	26	28.6	16	11	US-11-056-950-212	Sequence 212, App
20	26	28.6	16	11	US-11-056-950-216	Sequence 216, App
21	26	28.6	16	11	US-11-056-950-223	Sequence 223, App
22	26	28.6	16	11	US-11-223-699A-11	Sequence 11, Appl
23	26	28.6	16	11	US-11-121-566A-11	Sequence 11, Appl
24	26	28.6	16	11	US-11-152-974A-222	Sequence 222, App
25	26	28.6	16	11	US-11-153-143A-222	Sequence 222, App
26	25	27.5	16	11	US-11-056-950-30	Sequence 30, Appl
27	24	26.4	16	11	US-11-152-846-11	Sequence 11, Appl
28	24	26.4	16	11	US-11-207-078-103	Sequence 103, App
29	23.5	25.8	16	11	US-11-209-289-11	Sequence 11, Appl
30	23	25.3	16	9	US-10-461-904-2	Sequence 2, Appli
31	23	25.3	16	10	US-11-176-182-67	Sequence 67, Appl
32	23	25.3	16	11	US-11-152-846-2	Sequence 2, Appli
33	23	25.3	16	11	US-11-252-479-117	Sequence 117, App
34	22	24.2	16	9	US-10-834-397-238	Sequence 238, App
35	22	24.2	16	9	US-10-993-543-292	Sequence 292, App
36	22	24.2	16	11	US-11-106-415-15	Sequence 15, Appl
37	22	24.2	16	11	US-11-106-415-411	Sequence 411, App
38	22	24.2	16	11	US-11-233-256-15	Sequence 15, Appl
39	22	24.2	16	11	US-11-233-256-411	Sequence 411, App
40	21	23.1	16	9	US-10-201-525-40	Sequence 40, Appl
41	21	23.1	16	11	US-11-089-764-47	Sequence 47, Appl
42	21	23.1	16	11	US-11-054-515-2163	Sequence 2163, Ap
43	21	23.1	16	11	US-11-054-515-2838	Sequence 2838, Ap
44	21	23.1	16	11	US-11-054-515-3006	Sequence 3006, Ap
45	21	23.1	16	11	US-11-152-697-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-10-973-977-44
; Sequence 44, Application US/10973977
; Publication No. US20060008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973,977
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-973-977-44

Query Match 40.7%; Score 37; DB 9; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15
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RESULT 2
US-10-973-977-67
; Sequence 67, Application US/10973977
; Publication No. US20060008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973,977

; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-977-67

Query Match 40.7%; Score 37; DB 9; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12
| |:: || :|
Db 5 NMWQEVGKAMY 15

RESULT 3
US-10-973-977-75
; Sequence 75, Application US/10973977
; Publication No. US20060008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973,977
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV-1
; OTHER INFORMATION: Th-dominant/subdominant CTL epitopes in MVA.
US-10-973-977-75

Query Match 40.7%; Score 37; DB 9; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12
| |:: || :|
Db 5 NMWQEVGKAMY 15

RESULT 4
US-10-973-977-89
; Sequence 89, Application US/10973977
; Publication No. US20060008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973,977
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV-1 Th-CTL
; OTHER INFORMATION: A2 p17 epitope (A2 Variants) in MVA
US-10-973-977-89

Query Match 40.7%; Score 37; DB 9; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12
| |:: || :|
Db 5 NMWQEVGKAMY 15

RESULT 5
US-11-045-024-14479
; Sequence 14479, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney,John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14479
; LENGTH: 16
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY
US-11-045-024-14479

Query Match 40.7%; Score 37; DB 11; Length 16;
Best Local Similarity 45.5%; Pred. No. 6.4;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLY 12
| |:: || :|
Db 6 NMWQEVGKAMY 16

```
RESULT 6
US-11-115-425-88
; Sequence 88, Application US/11115425
; Publication No. US20060018881A1
;  GENERAL INFORMATION:
;       APPLICANT: Shiver, John W
;                  Liu, Margaret A
;                  Perry, Helen C
;       TITLE OF INVENTION: COORDINATE IN VIVO GENE EXPRESSION
;       NUMBER OF SEQUENCES: 100
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: J. Mark Hand
;            STREET: 126 Lincoln Avenue, P.O. Box 2000
;            CITY: Rahway
;            STATE: New Jersey
;            COUNTRY: United States of America
;            ZIP: 07065
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/11/115,425
;            FILING DATE: 27-Apr-2005
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hand, J. Mark
;            REGISTRATION NUMBER: 36,545
;            REFERENCE/DOCKET NUMBER: 19188YCB
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (732) 594-3905
;            TELEFAX: (732) 594-4720
;  INFORMATION FOR SEQ ID NO: 88:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 16 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       FRAGMENT TYPE: internal
;       SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-11-115-425-88

  Query Match             40.7%;  Score 37;  DB 11;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 6.4;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 7
US-11-185-907-11
; Sequence 11, Application US/11185907
; Publication No. US20060058233A1
; GENERAL INFORMATION:
;  APPLICANT: Elan Pharmaceuticals, Inc.
;  APPLICANT:  Regents of the University of California
;  APPLICANT:  Schenk, Dale B.
;  APPLICANT:  Masliah, Eliezer
;  APPLICANT:  Buttini, Manuel
;  APPLICANT:  Chilcote, Tamie
;  TITLE OF INVENTION: PREVENTION AND TREATMENT OF SYNUCLEINOPATHIC DISEASE
;  FILE REFERENCE: 015270-008950US
;  CURRENT APPLICATION NUMBER: US/11/185,907
;  CURRENT FILING DATE:  2005-07-19
;  PRIOR APPLICATION NUMBER: US 10/915,214
;  PRIOR FILING DATE: 2004-08-09
;  PRIOR APPLICATION NUMBER: US 10/699,517
;  PRIOR FILING DATE: 2003-10-31
;  PRIOR APPLICATION NUMBER: US 10/698,099
;  PRIOR FILING DATE: 2003-10-31
;  PRIOR APPLICATION NUMBER: US 60/423,012
;  PRIOR FILING DATE: 2002-11-01
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus
US-11-185-907-11

  Query Match             40.7%;  Score 37;  DB 11;  Length 16;
  Best Local Similarity   45.5%;  Pred. No. 6.4;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              | |:: || :|
Db          5 NMWQEVGKAMY 15


RESULT 8
US-11-056-950-226
; Sequence 226, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
;  APPLICANT: MICHELITSCH, Melissa D
;  TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
;  FILE REFERENCE: 2300-21026.20
;  CURRENT APPLICATION NUMBER: US/11/056,950
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: 10/917,646
;  PRIOR FILING DATE: 2004-08-13
;  PRIOR APPLICATION NUMBER: 60/586,509
;  PRIOR FILING DATE: 2004-07-09
;  PRIOR APPLICATION NUMBER: 60/570,368
;  PRIOR FILING DATE: 2004-05-12
;  PRIOR APPLICATION NUMBER: 60/494,962
;  PRIOR FILING DATE: 2003-08-13
;  NUMBER OF SEQ ID NOS: 260
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 226
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: peptide
US-11-056-950-226

  Query Match             35.2%;  Score 32;  DB 11;  Length 16;
  Best Local Similarity   35.7%;  Pred. No. 44;
  Matches    5;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLYNVE 15
              |:|  | |   |::
Db          3 NQWNKPSKPKTNMK 16


RESULT 9
US-11-056-950-230
; Sequence 230, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
;  APPLICANT: MICHELITSCH, Melissa D
;  TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
;  FILE REFERENCE: 2300-21026.20
;  CURRENT APPLICATION NUMBER: US/11/056,950
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: 10/917,646
;  PRIOR FILING DATE: 2004-08-13
;  PRIOR APPLICATION NUMBER: 60/586,509
```

; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 230
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
US-11-056-950-230

Query Match 35.2%; Score 32; DB 11; Length 16;
Best Local Similarity 35.7%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLYNVE 15
|:| | | |::
Db 2 NQWNKPSKPKTNMK 15

RESULT 10
US-11-056-950-234
; Sequence 234, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 234
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
US-11-056-950-234

Query Match 35.2%; Score 32; DB 11; Length 16;
Best Local Similarity 35.7%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLYNVE 15
|:| | | |::
Db 1 NQWNKPSKPKTNMK 14

RESULT 11
US-11-056-950-241
; Sequence 241, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 241
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
US-11-056-950-241

Query Match 35.2%; Score 32; DB 11; Length 16;
Best Local Similarity 35.7%; Pred. No. 44;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLYNVE 15
|:| | | |::
Db 1 NQWNKPSKPKTNMK 14

RESULT 12
US-11-056-950-54
; Sequence 54, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
; APPLICANT: MICHELITSCH, Melissa D
; TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
; FILE REFERENCE: 2300-21026.20
; CURRENT APPLICATION NUMBER: US/11/056,950
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 10/917,646
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/586,509
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/570,368
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/494,962
; PRIOR FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 54
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
US-11-056-950-54

Query Match 33.0%; Score 30; DB 11; Length 16;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 NRWEDPGKQLYN 13
|:| | | |
Db 5 NQWNKPSKPKTN 16

RESULT 13
US-10-530-061-1652
; Sequence 1652, Application US/10530061
; Publication No. US20060079453A1
; GENERAL INFORMATION:
; APPLICANT: SIDNEY, JOHN
; APPLICANT: SOUTHWOOD, SCOTT
; APPLICANT: SETTE, ALESSANDRO
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; FILE REFERENCE: 2060.033US02/EKS/M-M
; CURRENT APPLICATION NUMBER: US/10/530,061

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;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/US03/31308
;  PRIOR FILING DATE: 2003-10-03
;  PRIOR APPLICATION NUMBER: 60/416,207
;  PRIOR FILING DATE: 2002-10-03
;  PRIOR APPLICATION NUMBER: 60/417,269
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 2503
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1652.
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus
US-10-530-061-1652

  Query Match             30.8%;  Score 28;  DB 9;  Length 16;
  Best Local Similarity   57.1%;  Pred. No. 2e+02;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 WEDPGKQ 10
              |  || |
Db          4 WNHPGSQ 10


RESULT 14
US-11-056-950-185
; Sequence 185, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
;  APPLICANT: MICHELITSCH, Melissa D
;  TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
;  FILE REFERENCE: 2300-21026.20
;  CURRENT APPLICATION NUMBER: US/11/056,950
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: 10/917,646
;  PRIOR FILING DATE: 2004-08-13
;  PRIOR APPLICATION NUMBER: 60/586,509
;  PRIOR FILING DATE: 2004-07-09
;  PRIOR APPLICATION NUMBER: 60/570,368
;  PRIOR FILING DATE: 2004-05-12
;  PRIOR APPLICATION NUMBER: 60/494,962
;  PRIOR FILING DATE: 2003-08-13
;  NUMBER OF SEQ ID NOS: 260
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 185
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: peptide
US-11-056-950-185

  Query Match             29.7%;  Score 27;  DB 11;  Length 16;
  Best Local Similarity   28.6%;  Pred. No. 3e+02;
  Matches    4;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLYNVE 15
              ::|  | |   |::
Db          3 SQWNKPSKPKTNMK 16


RESULT 15
US-11-056-950-189
; Sequence 189, Application US/11056950
; Publication No. US20060035242A1
; GENERAL INFORMATION:
;  APPLICANT: MICHELITSCH, Melissa D
;  TITLE OF INVENTION: PRION-SPECIFIC PEPTIDE REAGENTS
;  FILE REFERENCE: 2300-21026.20
;  CURRENT APPLICATION NUMBER: US/11/056,950
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: 10/917,646
;  PRIOR FILING DATE: 2004-08-13
;  PRIOR APPLICATION NUMBER: 60/586,509
;  PRIOR FILING DATE: 2004-07-09
;  PRIOR APPLICATION NUMBER: 60/570,368
;  PRIOR FILING DATE: 2004-05-12
;  PRIOR APPLICATION NUMBER: 60/494,962
;  PRIOR FILING DATE: 2003-08-13
;  NUMBER OF SEQ ID NOS: 260
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 189
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: peptide
US-11-056-950-189

  Query Match             29.7%;  Score 27;  DB 11;  Length 16;
  Best Local Similarity   28.6%;  Pred. No. 3e+02;
  Matches    4;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLYNVE 15
              ::|  | |   |::
Db          2 SQWNKPSKPKTNMK 15


Search completed: May 15, 2006, 16:54:13
Job time : 27 secs
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OM protein - protein search, using sw model

Run on: May 15, 2006, 16:35:21 ; Search time 38 Seconds
(without alignments)
40.512 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 250

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	30.8	16	2	G24304	ribosomal protein
2	23	25.3	16	2	A31963	pyruvate dehydroge
3	22	24.2	16	2	PT0282	Ig heavy chain CDR
4	20	22.0	16	1	MTDFBS	melanotropin beta
5	19	20.9	16	2	D49021	Ig heavy chain J7
6	19	20.9	16	2	PL0137	protein kinase, 80
7	19	20.9	16	2	B44896	heat shock protein
8	18	19.8	16	2	B47014	orf2 3' of chuR -
9	18	19.8	16	2	PH0773	T-cell receptor be
10	18	19.8	16	2	A48630	bothrojaracin - ja
11	18	19.8	16	2	S13898	alkaline phosphata
12	17	18.7	16	2	B60560	formyltetrahydrofo
13	17	18.7	16	2	PH0137	T-cell receptor be
14	17	18.7	16	2	A49255	T-cell receptor be
15	17	18.7	16	2	B28587	T-cell receptor be
16	17	18.7	16	2	F53284	T-cell receptor be
17	17	18.7	16	2	PH1604	Ig H chain V-D-J r
18	17	18.7	16	2	PC1299	subtilisin (EC 3.4
19	17	18.7	16	2	A59155	multicystatin - to
20	17	18.7	16	2	S38292	30K allergen - rye
21	16	17.6	16	2	C45143	protein-tyrosine-p
22	16	17.6	16	2	H41299	T-cell receptor al
23	16	17.6	16	2	E53284	T-cell receptor be
24	16	17.6	16	2	D49037	TcR delta chain V-
25	16	17.6	16	2	S42237	hypothetical prote
26	16	17.6	16	2	A20190	hypodermin B - ear
27	16	17.6	16	2	S54271	GATA-2 protein - A
28	16	17.6	16	4	I79565	hypothetical TCL3/
29	15	16.5	16	2	A29541	little gastrin - C
30	15	16.5	16	2	PH0759	T-cell receptor be
31	15	16.5	16	2	A45454	ankyrin-binding gl
32	15	16.5	16	2	S11760	flgL protein - Cau
33	15	16.5	16	2	I51879	cystathionine beta
34	15	16.5	16	2	C37290	homeotic protein G
35	14.5	15.9	16	2	PH0791	T-cell receptor al
36	14	15.4	16	2	A59042	alpha-conotoxin Ep
37	14	15.4	16	2	S03532	Ig heavy chain J r
38	14	15.4	16	2	A28144	ribosomal protein
39	14	15.4	16	2	S34444	blaZ protein - Sta
40	14	15.4	16	2	S28213	glutathione transf
41	14	15.4	16	2	PT0237	Ig heavy chain CDR
42	14	15.4	16	2	G24687	T-cell receptor be
43	14	15.4	16	2	E58503	superoxide dismuta
44	14	15.4	16	2	B44820	7K protein - Esche
45	14	15.4	16	2	A49226	major outer membra

ALIGNMENTS

RESULT 1
G24304
ribosomal protein H [validated] - Haloarcula marismortui (fragment)
C;Species: Haloarcula marismortui
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jul-2000
C;Accession: G24304
R;Shoham, M.; Dijk, J.; Reinhardt, R.; Wittmann-Liebold, B.
FEBS Lett. 204, 323-330, 1986
A;Title: Purification and characterization of ribosomal proteins from the 30 S subunit
A;Reference number: A24304
A;Accession: G24304
A;Molecule type: protein
A;Residues: 1-16 <SHO>
A;Cross-references: UNIPARC:UPI000017AEA2
C;Keywords: protein biosynthesis; ribosome

Query Match 30.8%; Score 28; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          7 PGKQLYNVE 15
              || : || |
Db          1 PGNKYYNDE 9
```

RESULT 2
A31963
pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain type I - pig roundworm (fra
C;Species: Ascaris suum (pig roundworm)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: A31963
R;Thissen, J.; Komuniecki, R.
J. Biol. Chem. 263, 19092-19097, 1988
A;Title: Phosphorylation and inactivation of the pyruvate dehydrogenase from the anaero
A;Reference number: A31963; MUID:89066711; PMID:3198613
A;Accession: A31963
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <THI>
A;Cross-references: UNIPROT:P26267; UNIPARC:UPI000017B69C
C;Keywords: mitochondrion; oxidoreductase; phosphoprotein

Query Match 25.3%; Score 23; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          6 DPGKQLY 12
              |||   |
Db          9 DPGTSSY 15
```

RESULT 3

```
PT0282
Ig heavy chain CDR3 region (clone 4-94A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0282
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0282
A;Molecule type: DNA
A;Residues: 1-16 <YAM>
A;Cross-references: UNIPARC:UPI000017C1DA
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

  Query Match             24.2%;  Score 22;  DB 2;  Length 16;
  Best Local Similarity   57.1%;  Pred. No. 2.7e+03;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 WEDPGKQ 10
              | ||  |
Db          8 WFDPWGQ 14


RESULT 4
MTDFBS
melanotropin beta - spiny dogfish
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C;Accession: A01471
R;Bennett, H.P.J.; Lowry, P.J.; McMartin, C.; Scott, A.P.
Biochem. J. 141, 439-444, 1974
A;Title: Structural studies of alpha-melanocyte-stimulating hormone and a novel beta-mel
A;Reference number: A90277; MUID:75127390; PMID:4375978
A;Accession: A01471
A;Molecule type: protein
A;Residues: 1-16 <BEN>
A;Cross-references: UNIPROT:P01207; UNIPARC:UPI000012F1C2
C;Superfamily: corticotropin-lipotropin
C;Keywords: hormone

  Query Match             22.0%;  Score 20;  DB 1;  Length 16;
  Best Local Similarity   60.0%;  Pred. No. 5.8e+03;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 RWEDP 7
              ||  |
Db         11 RWSVP 15


RESULT 5
D49021
Ig heavy chain J7 region - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: D49021
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation
A;Reference number: A47624; MUID:90237760; PMID:2110243
A;Accession: D49021
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-16 <HAI>
A;Cross-references: UNIPARC:UPI000017692C
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             20.9%;  Score 19;  DB 2;  Length 16;
  Best Local Similarity   75.0%;  Pred. No. 8.4e+03;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RWED 6
              || |
Db          1 RWFD 4


RESULT 6
PL0137
protein kinase, 80K - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
C;Accession: PL0137
R;Dechert, U.; Weber, M.; Weber-Schaeuffelen, M.; Wollny, E.
J. Neurochem. 53, 1268-1275, 1989
A;Title: Isolation and partial characterization of an 80,000-dalton protein kinase from
A;Reference number: PL0137; MUID:89361455; PMID:2769266
A;Accession: PL0137
A;Molecule type: protein
A;Residues: 1-16 <DEC>
A;Cross-references: UNIPARC:UPI0000177D3E
C;Comment: This protein has a novel serine/threonine-specific protein kinase activity.

  Query Match             20.9%;  Score 19;  DB 2;  Length 16;
  Best Local Similarity   80.0%;  Pred. No. 8.4e+03;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 EDPGK 9
              || ||
Db         12 EDLGK 16


RESULT 7
B44896
heat shock protein 18 - Streptomyces albus (fragment)
C;Species: Streptomyces albus
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B44896
R;Guglielmi, G.; Mazodier, P.; Thompson, C.J.; Davies, J.
J. Bacteriol. 173, 7374-7381, 1991
A;Title: A survey of the heat shock response in four Streptomyces species reveals two g
A;Reference number: A44896; MUID:92041638; PMID:1682303
A;Accession: B44896
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <GUG>
A;Cross-references: UNIPROT:Q9R663; UNIPARC:UPI000017AD8C
A;Note: sequence extracted from NCBI backbone (NCBIP:65107)

  Query Match             20.9%;  Score 19;  DB 2;  Length 16;
  Best Local Similarity   50.0%;  Pred. No. 8.4e+03;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 WEDPGKQL 11
              :|: | ||
Db          6 YENLGAQL 13


RESULT 8
B47014
orf2 3' of chuR - Bacteroides thetaiotaomicron (fragment)
C;Species: Bacteroides thetaiotaomicron
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: B47014
R;Cheng, Q.; Hwa, V.; Salyers, A.A.
J. Bacteriol. 174, 7185-7193, 1992
A;Title: A locus that contributes to colonization of the intestinal tract by Bacteroide
A;Reference number: A47014; MUID:93054330; PMID:1429442
A;Accession: B47014
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-16 <CHE>
A;Cross-references: UNIPARC:UPI000017AB49
A;Note: sequence extracted from NCBI backbone (NCBIN:118015, NCBIP:118017)
```

```
  Query Match             19.8%;  Score 18;  DB 2;  Length 16;
  Best Local Similarity   60.0%;  Pred. No. 1.2e+04;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 KQLYN 13
              : |||
Db         12 QDLYN 16


RESULT 9
PH0773
T-cell receptor beta chain (C7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0773
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0773
A;Molecule type: mRNA
A;Residues: 1-16 <CAS>
A;Cross-references: UNIPARC:UPI0000115FC0; EMBL:X60868; NID:g50247; PIDN:CAA43257.1; PID
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

  Query Match             19.8%;  Score 18;  DB 2;  Length 16;
  Best Local Similarity   50.0%;  Pred. No. 1.2e+04;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    4;  Gaps    1;

Qy          7 PGK----QLY 12
              ||:    |||
Db          5 PGQGLTGQLY 14


RESULT 10
A48630
bothrojaracin - jararaca (fragment)
N;Alternate names: thrombin inhibitor
C;Species: Bothrops jararaca (jararaca)
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48630
R;Zingali, R.B.; Jandrot-Perrus, M.; Guillin, M.C.; Bon, C.
Biochemistry 32, 10794-10802, 1993
A;Title: Bothrojaracin, a new thrombin inhibitor isolated from Bothrops jararaca venom:
A;Reference number: A48630; MUID:94002075; PMID:8399228
A;Accession: A48630
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <ZIN>
A;Cross-references: UNIPROT:Q9PRZ4; UNIPARC:UPI00000FD244
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:138787)

  Query Match             19.8%;  Score 18;  DB 2;  Length 16;
  Best Local Similarity   33.3%;  Pred. No. 1.2e+04;
  Matches    3;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 WEDPGKQLY 12
              |   |:  |
Db          6 WSPYGQGCY 14


RESULT 11
S13898
alkaline phosphatase (EC 3.1.3.1) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S13898
R;Fujimori-Arai, Y.; Koyama, I.; Hirano, K.; Sakagishi, Y.; Komoda, T.
Arch. Biochem. Biophys. 284, 320-325, 1991
A;Title: Purification and partial characterization of intestinal-like alkaline phosphata
A;Reference number: S13898; MUID:91112827; PMID:1989515
A;Accession: S13898
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <FUJ>
A;Cross-references: UNIPROT:Q7M2K8; UNIPARC:UPI000017C5B6
C;Keywords: phosphoric monoester hydrolase

  Query Match             19.8%;  Score 18;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 EDP 7
              |||
Db          7 EDP 9


RESULT 12
B60560
formyltetrahydrofolate dehydrogenase (EC 1.5.1.6) / aldehyde dehydrogenase (NADP) (EC 1
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 31-Dec-2004
C;Accession: B60560
R;Johlin, F.C.; Swain, E.; Smith, C.; Tephly, T.R.
Mol. Pharmacol. 35, 745-750, 1989
A;Title: Studies on the mechanism of methanol poisoning: purification and comparison of
A;Reference number: A60560; MUID:89281497; PMID:2733692
A;Accession: B60560
A;Molecule type: protein
A;Residues: 1-16 <JOH>
A;Cross-references: UNIPROT:Q8TBP8; UNIPARC:UPI000017CE07
C;Superfamily: 10-formyltetrahydrofolate dehydrogenase
C;Keywords: multifunctional enzyme; NADP; oxidoreductase

  Query Match             18.7%;  Score 17;  DB 2;  Length 16;
  Best Local Similarity   40.0%;  Pred. No. 1.8e+04;
  Matches    2;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GKQLY 12
              |:::|
Db         12 GQEVY 16


RESULT 13
PH0137
T-cell receptor beta chain V-D-J region MS20 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997
C;Accession: PH0137
R;Martin, R.; Howell, M.D.; Jaraquemada, D.; Flerlage, M.; Richert, J.; Brostoff, S.; Lo
J. Exp. Med. 173, 19-24, 1991
A;Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the conte
A;Reference number: PH0135; MUID:91086843; PMID:1702137
A;Accession: PH0137
A;Molecule type: mRNA
A;Residues: 1-16 <MAR>
A;Cross-references: UNIPARC:UPI000017C3AF
C;Keywords: T-cell receptor

  Query Match             18.7%;  Score 17;  DB 2;  Length 16;
  Best Local Similarity   27.3%;  Pred. No. 1.8e+04;
  Matches    3;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 NRWEDPGKQLY 12
              :| : |   |:
Db          6 SRKDSPSSPLH 16


RESULT 14
A49255
T-cell receptor beta chain V-D-J-C region (V beta 7, J beta 1.6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
```

```
C;Accession: A49255
R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using
A;Reference number: A49039; MUID:92164737; PMID:1311263
A;Accession: A49255
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-16 <ROS>
A;Cross-references: UNIPARC:UPI000017C3B9
A;Note: sequence extracted from NCBI backbone (NCBIP:90722)
C;Keywords: T-cell receptor

  Query Match             18.7%;  Score 17;  DB 2;  Length 16;
  Best Local Similarity   75.0%;  Pred. No. 1.8e+04;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 PGKQ 10
              || |
Db          6 PGTQ 9


RESULT 15
B28587
T-cell receptor beta-2 chain J-B2.3 segment - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C;Accession: B28587
R;Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A;Title: Organization and sequences of the diversity, joining, and constant region genes
A;Reference number: A94081; MUID:86094276; PMID:3866244
A;Accession: B28587
A;Molecule type: DNA
A;Residues: 1-16 <TOY>
A;Cross-references: UNIPARC:UPI000002FD06; GB:M14159; NID:g338852; PIDN:AAA60677.1; PID:
C;Keywords: T-cell receptor

  Query Match             18.7%;  Score 17;  DB 2;  Length 16;
  Best Local Similarity   60.0%;  Pred. No. 1.8e+04;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 PGKQL 11
              || :|
Db          9 PGTRL 13


Search completed: May 15, 2006, 16:39:41
Job time : 39 secs
```

GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 15, 2006, 16:34:51 ; Search time 224 Seconds
(without alignments)
50.395 Million cell updates/sec

Title: US-09-865-281A-1
Perfect score: 91
Sequence: 1 KNRWEDPGKQLYNVEA 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1144

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	27.5	16	2	Q7DLY3_SOLTU	Q7dly3 solanum tub
2	22	24.2	16	1	FIBA_RABIT	P14461 oryctolagus
3	22	24.2	16	2	Q9TWC0_ACACA	Q9twc0 acanthamoeb
4	22	24.2	16	2	Q4TSR1_9SPHN	Q4tsr1 erythrobact
5	22	24.2	16	2	Q691Z1_ANOSA	Q691z1 anolis sagr
6	21	23.1	16	2	O21922_9CAUD	O21922 streptococc
7	20	22.0	16	1	MLB_SQUAC	P01207 squalus aca
8	20	22.0	16	2	Q9UR86_CANPA	Q9ur86 candida par
9	20	22.0	16	2	Q9NY32_HUMAN	Q9ny32 homo sapien
10	19.5	21.4	16	2	Q7WZ27_PSEAE	Q7wz27 pseudomonas
11	19	20.9	16	2	Q9UCW4_HUMAN	Q9ucw4 homo sapien
12	19	20.9	16	2	Q5C7F3_SCHJA	Q5c7f3 schistosoma
13	19	20.9	16	2	Q7SM54_9DELA	Q7sm54 human t-lym
14	18	19.8	16	2	Q53SB3_HUMAN	Q53sb3 homo sapien
15	18	19.8	16	2	Q7M2K8_RABIT	Q7m2k8 oryctolagus
16	18	19.8	16	2	Q9T2Q6_SOLTU	Q9t2q6 solanum tub
17	18	19.8	16	2	Q4QYV4_SACOF	Q4qyv4 saccharum o
18	18	19.8	16	2	Q5MG28_COETO	Q5mg28 coeligena t
19	18	19.8	16	2	Q9PRZ4_BOTJA	Q9prz4 bothrops ja
20	17.5	19.2	16	1	AFP2S_MALPA	P83142 malva parvi
21	17	18.7	16	1	SAL3_ONCMY	P82240 oncorhynchu
22	17	18.7	16	2	Q7S047_NEUCR	Q7s047 neurospora
23	17	18.7	16	2	Q8MM83_9NEOP	Q8mm83 heliconius
24	17	18.7	16	2	Q8MM84_9NEOP	Q8mm84 heliconius
25	17	18.7	16	2	Q8MM85_9NEOP	Q8mm85 heliconius
26	17	18.7	16	2	Q8MUN3_9NEOP	Q8mun3 heliconius
27	17	18.7	16	2	Q8MUN5_9NEOP	Q8mun5 heliconius
28	17	18.7	16	2	Q4X8S1_PLACH	Q4x8s1 plasmodium
29	17	18.7	16	2	Q95M79_HORSE	Q95m79 equus cabal
30	17	18.7	16	2	Q9TR88_BOVIN	Q9tr88 bos taurus
31	17	18.7	16	2	Q7M1V9_LYCES	Q7m1v9 lycopersico
32	17	18.7	16	2	Q7M263_SECCE	Q7m263 secale cere
33	17	18.7	16	2	Q10748_CLOTM	Q10748 clostridium
34	17	18.7	16	2	Q9R557_BACSP	Q9r557 bacillus sp
35	17	18.7	16	2	Q9R5C1_NITEU	Q9r5c1 nitrosomona
36	17	18.7	16	2	Q7ZGT5_9HIV1	Q7zgt5 human immun
37	16	17.6	16	1	SSIT_STRMB	P83544 streptomyce
38	16	17.6	16	2	Q15632_HUMAN	Q15632 homo sapien
39	16	17.6	16	2	Q6DTV5_HUMAN	Q6dtv5 homo sapien
40	16	17.6	16	2	Q96RT5_HUMAN	Q96rt5 homo sapien
41	16	17.6	16	2	Q9UCH1_HUMAN	Q9uch1 homo sapien
42	16	17.6	16	2	Q5BR47_SCHJA	Q5br47 schistosoma
43	16	17.6	16	2	Q86CU9_9DIPT	Q86cu9 drosophila
44	16	17.6	16	2	Q86FV2_DROAE	Q86fv2 drosophila
45	16	17.6	16	2	Q7RA58_PLAYO	Q7ra58 plasmodium

ALIGNMENTS

RESULT 1
Q7DLY3_SOLTU
ID Q7DLY3_SOLTU PRELIMINARY; PRT; 16 AA.
AC Q7DLY3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-fructofuranosidase (Invertase) (EC 3.2.1.26) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96279736; PubMed=8710506; DOI=10.1093/nar/24.12.2347;
RA Bournay A.S., Hedley P.E., Maddison A., Waugh R., Machray G.C.;
RT "Exon skipping induced by cold stress in a potato invertase gene
RT transcript.";
RL Nucleic Acids Res. 24:2347-2351(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Maddison A.L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X95820; CAA65086.1; -; Genomic_DNA.
DR GO; GO:0004564; F:beta-fructofuranosidase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
KW Glycosidase; Hydrolase.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1894 MW; 003053E73810C336 CRC64;

Query Match 27.5%; Score 25; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 KNRWEDPGKQLY 12
              ||   ||   :|
Db          2 KNWINDPNAPMY 13
```

RESULT 2
FIBA_RABIT
ID FIBA_RABIT STANDARD; PRT; 16 AA.
AC P14461;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;

```
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   PROTEIN SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
CC       nonidentical chains (alpha, beta and gamma). The 2 heterotrimers
CC       are in head to head conformation with the N-termini in a small
CC       central domain (By similarity).
CC   -!- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC       chains connects the central nodule to the C-terminal domains
CC       (distal nodules). The long C-terminal ends of the alpha chains
CC       fold back, contributing a fourth strand to the coiled coil
CC       structure.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
KW   Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
FT   PEPTIDE       1     16       Fibrinopeptide A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1651 MW;  DFB623279EA55EB6 CRC64;

  Query Match             24.2%;  Score 22;  DB 1;  Length 16;
  Best Local Similarity   42.9%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 DPGKQLY 12
              |||:  :
Db          2 DPGESTF 8


RESULT 3
Q9TWC0_ACACA
ID   Q9TWC0_ACACA  PRELIMINARY;      PRT;    16 AA.
AC   Q9TWC0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   Actin (Fragment).
OS   Acanthamoeba castellanii (Amoeba).
OC   Eukaryota; Acanthamoebidae; Acanthamoeba.
OX   NCBI_TaxID=5755;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=95014701; PubMed=7929556; DOI=10.1083/jcb.127.1.107;
RA   Machesky L.M., Atkinson S.J., Ampe C., Vandekerckhove J.,
RA   Pollard T.D.;
RT   "Purification of a cortical complex containing two unconventional
RT   actins from Acanthamoeba by affinity chromatography on profilin-
RT   agarose.";
RL   J. Cell Biol. 127:107-115(1994).
SQ   SEQUENCE   16 AA;  2115 MW;  A64E248880BA06C4 CRC64;

  Query Match             24.2%;  Score 22;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 WED 6
              |||
Db          2 WED 4


RESULT 4
Q4TSR1_9SPHN
ID   Q4TSR1_9SPHN PRELIMINARY;      PRT;    16 AA.
AC   Q4TSR1;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=ELI0115;
OS   Erythrobacter litoralis HTCC2594.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC   Sphingomonadaceae; Erythrobacter.
OX   NCBI_TaxID=314225;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=HTCC2594;
RA   Giovannoni S.J., Cho J.-C., Ferriera S., Johnson J., Kravitz S.,
RA   Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,
RA   Friedman R., Venter J.C.;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAGG01000001; EAL76309.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   16 AA;  1864 MW;  4D15F5FE0BA28A1E CRC64;

  Query Match             24.2%;  Score 22;  DB 2;  Length 16;
  Best Local Similarity   75.0%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RWED 6
              || |
Db          2 RWRD 5


RESULT 5
Q691Z1_ANOSA
ID   Q691Z1_ANOSA PRELIMINARY;      PRT;    16 AA.
AC   Q691Z1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
OS   Anolis sagrei (Brown anole).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX   NCBI_TaxID=38937;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15356629; DOI=10.1038/nature02807;
RA   Kolbe J.J., Glor R.E., Rodriguez Schettino L., Chamizo Lara A.,
RA   Larson A., Losos J.B.;
RT   "Genetic variation increases during biological invasion by a Cuban
RT   lizard.";
RL   Nature 431:177-181(2004).
DR   EMBL; AY655188; AAT78035.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000883; COX1.
DR   PANTHER; PTHR10422; COX1; 1.
KW   Mitochondrion.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1953 MW;  B0C8C72FF7483A35 CRC64;

  Query Match             24.2%;  Score 22;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          2 NRW 4
              |||
Db          4 NRW 6


RESULT 6
O21922_9CAUD
ID   O21922_9CAUD PRELIMINARY;      PRT;    16 AA.
AC   O21922; O21923;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Integrase (Fragment).
GN   Name=int;
OS   Streptococcus thermophilus bacteriophage Sfi21.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX   NCBI_TaxID=64186;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98008989; PubMed=9344917; DOI=10.1006/viro.1997.8769;
RA   Bruttin A., Foley S., Brussow H.;
RT   "The site-specific integration system of the temperate Streptococcus
RT   thermophilus bacteriophage phiSfi21.";
RL   Virology 237:148-158(1997).
DR   EMBL; AF013584; AAC48909.1; -; Genomic_DNA.
DR   EMBL; AF013587; AAC48910.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   16 AA;  1856 MW;  8FA82D3270B9A959 CRC64;

  Query Match             23.1%;  Score 21;  DB 2;  Length 16;
  Best Local Similarity   33.3%;  Pred. No. 2.2e+04;
  Matches    3;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGK 9
              |  | : |:
Db          1 KQMWTECGR 9


RESULT 7
MLB_SQUAC
ID   MLB_SQUAC      STANDARD;      PRT;    16 AA.
AC   P01207;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Melanotropin beta.
OS   Squalus acanthias (Spiny dogfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Squaliformes; Squaloidei;
OC   Squalidae; Squalus.
OX   NCBI_TaxID=7797;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=75127390; PubMed=4375978;
RA   Bennett H.P.J., Lowry P.J., McMartin C., Scott A.P.;
RT   "Structural studies of alpha-melanocyte-stimulating hormone and a
RT   novel beta-melanocyte-stimulating hormone from the neurointermediate
RT   lobe of the pituitary of the dogfish Squalus acanthias.";
RL   Biochem. J. 141:439-444(1974).
CC   -!- SIMILARITY: Belongs to the POMC family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   PIR; A01471; MTDFBS.
KW   Direct protein sequencing; Hormone.
SQ   SEQUENCE   16 AA;  1939 MW;  993AF43C8A640A0E CRC64;

  Query Match             22.0%;  Score 20;  DB 1;  Length 16;
  Best Local Similarity   60.0%;  Pred. No. 3.3e+04;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 RWEDP 7
              ||  |
Db         11 RWSVP 15


RESULT 8
Q9UR86_CANPA
ID   Q9UR86_CANPA  PRELIMINARY;      PRT;    16 AA.
AC   Q9UR86;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   Class I cytochrome C isoform A (Fragment).
OS   Candida parapsilosis (Yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=5480;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=93305688; PubMed=8391313; DOI=10.1016/0005-2728(93)90135-3;
RA   Camougrand N., Velours J., Denis M., Guerin M.;
RT   "Isolation, characterization and function of the two cytochromes c of
RT   the yeast Candida parapsilosis.";
RL   Biochim. Biophys. Acta 1143:135-141(1993).
SQ   SEQUENCE   16 AA;  1646 MW;  762FF64F875F237B CRC64;

  Query Match             22.0%;  Score 20;  DB 2;  Length 16;
  Best Local Similarity   57.1%;  Pred. No. 3.3e+04;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 EDPGKQL 11
              | ||  |
Db          9 EKPGASL 15


RESULT 9
Q9NY32_HUMAN
ID   Q9NY32_HUMAN PRELIMINARY;      PRT;    16 AA.
AC   Q9NY32;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Homo sapiens IL1L1 interleukin-1 like protein 1, exons 1-6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20545212; PubMed=11093146;
RX   DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
RA   Barton J.L., Herbst R., Bosisio D., Higgins L., Nicklin M.J.H.;
RT   "A tissue specific IL-1 receptor antagonist homolog from the IL-1
RT   cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
RL   Eur. J. Immunol. 30:3299-3308(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Nicklin M.J.H.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ271338; CAB67703.1; -; Genomic_DNA.
SQ   SEQUENCE   16 AA;  1804 MW;  47FFF677F8B6D87E CRC64;

  Query Match             22.0%;  Score 20;  DB 2;  Length 16;
  Best Local Similarity   40.0%;  Pred. No. 3.3e+04;
  Matches    4;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 KNRWEDPGKQ 10
              : | |  ||:
Db          7 RGRKEGEGKE 16
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RESULT 10
Q7WZ27_PSEAE
ID   Q7WZ27_PSEAE PRELIMINARY;      PRT;    16 AA.
AC   Q7WZ27;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative radical activating enzyme (Fragment).
GN   Name=PA0975;
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PA14;
RX   PubMed=14983043; DOI=10.1073/pnas.0304622101;
RA   He J., Baldini R.L., Deziel E., Saucier M., Zhang Q., Liberati N.T.,
RA   Lee D., Urbach J., Goodman H.M., Rahme L.G.;
RT   "The broad host range pathogen Pseudomonas aeruginosa strain PA14
RT   carries two pathogenicity islands harboring plant and animal virulence
RT   genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:2530-2535(2004).
DR   EMBL; AY273870; AAP82945.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   16 AA;  1941 MW;  1DDD9B5D22AF6B7C CRC64;

  Query Match             21.4%;  Score 19.5;  DB 2;  Length 16;
  Best Local Similarity   66.7%;  Pred. No. 4.1e+04;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          4 WED-PG 8
              | | ||
Db         10 WNDEPG 15


RESULT 11
Q9UCW4_HUMAN
ID   Q9UCW4_HUMAN  PRELIMINARY;      PRT;    16 AA.
AC   Q9UCW4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   Dystrophin isoform (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=96081207; PubMed=8541829;
RA   Austin R.C., Howard P.L., D'Souza V.N., Klamut H.J., Ray P.N.;
RT   "Cloning and characterization of alternatively spliced isoforms of
RT   Dp71.";
RL   Hum. Mol. Genet. 4:1475-1483(1995).
SQ   SEQUENCE   16 AA;  1833 MW;  E0CFFAF3B5CB5BBF CRC64;

  Query Match             20.9%;  Score 19;  DB 2;  Length 16;
  Best Local Similarity   60.0%;  Pred. No. 5e+04;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 PGKQL 11
              ||| :
Db          7 PGKPM 11


RESULT 12
Q5C7F3_SCHJA
ID   Q5C7F3_SCHJA PRELIMINARY;      PRT;    16 AA.
AC   Q5C7F3;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC   Schistosomatoidea; Schistosomatidae; Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Han Z.;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY808532; AAX24421.1; -; mRNA.
KW   Hypothetical protein.
SQ   SEQUENCE   16 AA;  1945 MW;  7369A9EAB699AC65 CRC64;

  Query Match             20.9%;  Score 19;  DB 2;  Length 16;
  Best Local Similarity   75.0%;  Pred. No. 5e+04;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 LYNV 14
                :|||
Db          1 MYNV 4


RESULT 13
Q7SM54_9DELA
ID   Q7SM54_9DELA PRELIMINARY;      PRT;    16 AA.
AC   Q7SM54;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tax protein (Fragment).
OS   Human T-lymphotropic virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX   NCBI_TaxID=11908;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gonzalez Perez M.P., Garcia Saiz A.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF529962; AAP87693.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   16 AA;  1782 MW;  9CDDDFFE4146EA2F CRC64;

  Query Match             20.9%;  Score 19;  DB 2;  Length 16;
  Best Local Similarity   50.0%;  Pred. No. 5e+04;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 EDPGKQ 10
              | ||::
Db          4 EPPGEK 9


RESULT 14
Q53SB3_HUMAN
ID   Q53SB3_HUMAN PRELIMINARY;      PRT;    16 AA.
AC   Q53SB3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein SLC4A10 (Fragment).
GN   Name=SLC4A10;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Belter E., Kozlowicz A., Dixon R.;
RT   "The sequence of Homo sapiens BAC clone RP11-220I15.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
```

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RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.H.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Wilson R.K.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC062022; AAX93124.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1801 MW;  F5D5B8263B966EC8 CRC64;

  Query Match             19.8%;  Score 18;  DB 2;  Length 16;
  Best Local Similarity   42.9%;  Pred. No. 7.4e+04;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 EDPGKQL 11
              :| | |:
Db          4 KDQGAQM 10


RESULT 15
Q7M2K8_RABIT
ID   Q7M2K8_RABIT PRELIMINARY;      PRT;    16 AA.
AC   Q7M2K8;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Alkaline phosphatase (EC 3.1.3.1).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=91112827; PubMed=1989515;
RA   Fujimori-Arai Y., Koyama I., Hirano K., Sakagishi Y., Komoda T.;
RT   "Purification and partial characterization of intestinal-like alkaline
RT   phosphatase in rabbit kidney.";
RL   Arch. Biochem. Biophys. 284:320-325(1991).
DR   PIR; S13898; S13898.
DR   GO; GO:0004035; F:alkaline phosphatase activity; IEA.
SQ   SEQUENCE   16 AA;  1973 MW;  E9E78040172D8E38 CRC64;

  Query Match             19.8%;  Score 18;  DB 2;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 EDP 7
              |||
Db          7 EDP 9


Search completed: May 15, 2006, 16:38:59
Job time : 226 secs
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